

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Innogenetics sa.
- (B) STREET: Industriepark Zwijnaarde 7, box 4
- (C) CITY: Ghent
- (E) COUNTRY: Belgium
- (F) POSTAL CODE (ZIP): B-9052
- (G) TELEPHONE: 00 32 9 241 07 11
- (H) TELEFAX: 00 32 9 241 07 99

(ii) TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy.

(iii) NUMBER OF SEQUENCES: 270

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR34-4-20

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTC ACG GAA CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG
 Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
 1 5 10 15

48

GCC CAG TGT GGT TAT CGC CGC TGC CGT GCC AGT GGA GTT CTG CCT ACC
 Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr

96

20 96 30

25

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AGC TTC GGC AAC ACA ATC ACT TGC TAC ATC AAG GCC ACA GCG GCT GCA      144
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
      35                      40                      45

AGG GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTC TGC GGA GAT GAT      192
Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp
      50                      55                      60

CTG GTC GTG GTG GCT GAG AGT
Leu Val Val Val Ala Glu Ser      213
      65                      70

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
 1              5              10              15

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
      20              25              30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
      35              40              45

Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp
      50              55              60

Leu Val Val Val Ala Glu Ser
65              70

```

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR36-23-18

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTC	ACG	GAA	CGG	CTT	TAC	TGC	GGG	GGC	CCT	ATG	TTC	AAC	AGC	AAG	GGG	48
Leu	Thr	Glu	Arg	Leu	Tyr	Cys	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly	
1				5					10					15		
GCC	CAG	TGT	GGT	TAT	CGC	CGC	TGC	CGT	GCC	AGT	GGA	GTT	CTG	CCT	ACC	96
Ala	Gln	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Pro	Thr	
			20					25					30			
AGC	TTC	GGC	AAC	ACA	ATC	ACT	TGC	TAC	ATC	AAG	GCC	ACA	GCG	GCT	GCA	144
Ser	Phe	Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Ile	Lys	Ala	Thr	Ala	Ala	Ala	
			35				40					45				
AGG	GCC	GCA	GGC	CTC	CGG	AAC	CCG	GAC	TTT	CTT	GTC	TGC	GGA	GAT	GAT	192
Arg	Ala	Ala	Gly	Leu	Arg	Asn	Pro	Asp	Phe	Leu	Val	Cys	Gly	Asp	Asp	
			50			55					60					
CTG	GTC	GTG	GTG	GCT	GAG	AGT										213
Leu	Val	Val	Val	Ala	Glu	Ser										
65					70											

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Leu	Thr	Glu	Arg	Leu	Tyr	Cys	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly
1				5					10					15	
Ala	Gln	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Pro	Thr
			20					25					30		
Ser	Phe	Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Ile	Lys	Ala	Thr	Ala	Ala	Ala
			35				40					45			
Arg	Ala	Ala	Gly	Leu	Arg	Asn	Pro	Asp	Phe	Leu	Val	Cys	Gly	Asp	Asp
			50			55					60				
Leu	Val	Val	Val	Ala	Glu	Ser									
65					70										

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-23-18

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTT AAC AGC AAG GGG	48
Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly	
1 5 10 15	
GCC CAG TGT GGT TAT CGC CGT TGC CGT GCC AGT GGA GTT CTG CCT ACC	96
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr	
20 25 30	
AGC TTC GGC AAC ACA ATC ACT TGT TAC ATC AAA GCC ACA GCG GCC GCA	144
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala	
35 40 45	
AAA GCC GCA GGC CTC CGG AGC CCG GAC TTT CTT GTC TGC GGA GAT GAT	192
Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp	
50 55 60	
CTG GTC GTG GTG GCT GAG AGT	
Leu Val Val Val Ala Glu Ser	213
65 70	

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly	
1 5 10 15	
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr	
20 25 30	
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala	
35 40 45	

99

Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp
 50 55 60

Leu Val Val Val Ala Glu Ser
 65 70

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-23-20

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTT AAC AGC AAA GGG	48
Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly	
1 5 10 15	
GCC CAG TGT GGT TAT CGC CGT TGC CGT GCC AGT GGA GTT CTG CCT ACC	96
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr	
20 25 30	
AGC TTC GGC AAC ACA ATC ACT TGT TAC ATC AAA GCC ACA GCG GCC GCA	144
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala	
35 40 45	
AAA GCC GCA GGC CTC CGG AGC CCG GAC TTT CTT GTC TGC GGA GAT GAT	192
Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp	
50 55 60	
CTG GTC GTG GTG GCT GAG AGT	213
Leu Val Val Val Ala Glu Ser	
65 70	

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
 1      5      10      15
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
      20      25      30
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
      35      40      45
Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp
      50      55      60
Leu Val Val Val Ala Glu Ser
      65      70

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(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR33-2-17

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG      48
Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
 1      5      10      15
GCC CAG TGT GGT TAT CGC CGT TGT CGT GCC AGT GGA GTT CTG CCT ACC      96
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
      20      25      30
AGT TTC GGC AAC ACA ATC ACT TGT TAC ATC AAG GCC ACA GCG GCT GCA      144
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
      35      40      45
AAA GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTT TGC GGA GAT GAT      192

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101

Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp
 50 55 60

TTG GTC GTG GTG GCT GAG AGT
 Leu Val Val Val Ala Glu Ser
 65 70

213

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
 1 5 10 15

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
 20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
 35 40 45

Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp
 50 55 60

Leu Val Val Val Ala Glu Ser
 65 70

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR33-2-21

(ix) FEATURE:

- (A) NAME/KEY: CDS -
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG 48
 Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
 1 5 10 15

GCC CAG TGT GGT TAT CGC CGT TGT CGT GCC AGT GGA GTT CTG CCT ACC 96
 Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
 20 25 30

AGT TTC GGC AAC ACA ATC ACT TGT TAC ATC AAG GCC ACA GCG GCT GCA 144
 Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
 35 40 45

AAA GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTT TGC GGA GAT GAT 192
 Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp
 50 55 60

TTG GTC GTG GTG GCT GAG AGT 213
 Leu Val Val Val Ala Glu Ser
 65 70

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
 1 5 10 15

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
 20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
 35 40 45

Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp
 50 55 60

Leu Val Val Val Ala Glu Ser
 65 70

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: HD10-2-5(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAC ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGT AAT	286
Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCT GCG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AGG TAC	334
Thr Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATG TTG GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Met Leu Val	
115 120 125	
GGC GCG GCC ACG ATG TGC TCT GCT CTC TAC GTG GGT GAT ATG TGT GGC	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT	478
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	
145 150 155	
CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA	526
Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser	
160 165 170 175	

GGA CAC CGA ATG GCT
Gly His Arg Met Ala
180

541

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val
1 5 10 15
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly
20 25 30
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His
35 40 45
Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
50 55 60
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val
65 70 75 80
Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr
85 90 95
Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
100 105 110
Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Met Leu Val Gly
115 120 125
Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala
130 135 140
Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
145 150 155 160
Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
165 170 175
His Arg Met Ala
180

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 541 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-2-14

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

C	GTC	GGC	GCT	CCT	GTA	GGA	GGC	GTC	GCA	AGA	GCC	CTT	GCG	CAT	GGC	46
	Val	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	
	1				5					10					15	
GTG	AGG	GCC	CTT	GAA	GAC	GGG	ATA	AAT	TTC	GCA	ACA	GGG	AAT	TTG	CCC	94
Val	Arg	Ala	Leu	Glu	Asp	Gly	Ile	Asn	Phe	Ala	Thr	Gly	Asn	Leu	Pro	
				20					25					30		
GGT	TGC	TCC	TTT	TCT	ATC	TTC	CTT	CCT	GCT	CTG	TTC	TCT	TGC	TTA	ATC	142
Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Pro	Ala	Leu	Phe	Ser	Cys	Leu	Ile	
			35					40					45			
CAT	CCA	GCA	GCT	AGT	CTA	GAG	TGG	CGG	AAC	ACG	TCT	GGC	CTC	TAT	GTC	190
His	Pro	Ala	Ala	Ser	Leu	Glu	Trp	Arg	Asn	Thr	Ser	Gly	Leu	Tyr	Val	
		50					55					60				
CTT	ACC	AAC	GAC	TGT	TCC	AAT	AGC	AGT	ATT	GTG	TAT	GAG	GCC	GAT	GAC	238
Leu	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asp	
	65					70				75						
GTT	ATT	CTG	CAC	ACA	CCC	GGC	TGT	GTA	CCT	TGT	GTT	CAG	GAC	GGT	AAT	286
Val	Ile	Leu	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Gln	Asp	Gly	Asn	
	80				85				90					95		
ACA	TCT	GCG	TGC	TGG	ACC	CCA	GTG	ACA	CCT	ACA	GTG	GCA	GTC	AGG	TAC	334
Thr	Ser	Ala	Cys	Trp	Thr	Pro	Val	Thr	Pro	Thr	Val	Ala	Val	Arg	Tyr	
				100					105					110		
GTC	GGA	GCA	ACC	ACC	GCT	TCG	ATA	CGC	AGG	CAT	GTA	GAC	ATA	TTG	GTG	382
Val	Gly	Ala	Thr	Thr	Ala	Ser	Ile	Arg	Arg	His	Val	Asp	Ile	Leu	Val	
			115					120					125			
GGC	GCG	GCC	ACA	ATG	TGC	TCT	GCT	CTC	TAC	GTG	GGT	GAT	ATG	TGT	GGG	430
Gly	Ala	Ala	Thr	Met	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Met	Cys	Gly	
		130					135					140				
GCC	GTC	TTC	CTC	GTG	GGA	CAA	GCC	TTC	ACG	TTC	AGA	CCT	CGT	CGC	CAT	478
Ala	Val	Phe	Leu	Val	Gly	Gln	Ala	Phe	Thr	Phe	Arg	Pro	Arg	Arg	His	
	145					150					155					
CAA	ACG	GTC	CAG	ACC	TGT	AAC	TGC	TCA	CTG	TAC	CCA	GGC	CAT	CTT	TCA	526

Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser
 160 165 170 175

GGA CAC CGA ATG GCT
 Gly His Arg Met Ala
 180

541

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val
 1 5 10 15
 Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly
 20 25 30
 Cys Ser Phe Ser Ile Phe Leu Pro Ala Leu Phe Ser Cys Leu Ile His
 35 40 45
 Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
 50 55 60
 Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val
 65 70 75 80
 Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr
 85 90 95
 Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
 100 105 110
 Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val Gly
 115 120 125
 Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala
 130 135 140
 Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
 145 150 155 160
 Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
 165 170 175
 His Arg Met Ala
 180

(2) INFORMATION FOR SEQ ID NO: 17 :

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-2-21

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAC ACG TCT GGC CTC TAC GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGT AAT	286
Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCT GCG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AGG TAC	334
Thr Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATA TTG GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val	
115 120 125	
GGC GCG GCC ACG ATG TGC TCT GCT CTC TAC GTG GGT GAT ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	

GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT 478
 Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His
 145 150 155

CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA 526
 Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser
 160 165 170 175

GGA CAC CGA ATG GCT 541
 Gly His Arg Met Ala
 180

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val
 1 5 10 15

Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly
 20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His
 35 40 45

Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
 50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val
 65 70 75 80

Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr
 85 90 95

Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
 100 105 110

Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val Gly
 115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala
 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
 165 170 175

His Arg Met Ala

180

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR36-9-13

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATT TTC CTT CTT GCT CTG TTC TCT TGC TTA ATT	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAC GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGC ATA CCT TGT GTC CAG GAC GGC AAT	286
Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCC ACG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AAG TAC	334
Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr	
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val	
115 120 125	

GGC GCG GCC ACG ATG TGC TCA GCG CTC TAC GTG GGT GAT ATG TGT GGG Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	430
130 135 140	
GCC GTC TTC CTT GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	478
145 150 155	
CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser	526
160 165 170 175	
GGA CAT CGA ATG GCT Gly His Arg Met Ala	541
180	

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val	
1 5 10 15	
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly	
20 25 30	
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His	
35 40 45	
Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu	
50 55 60	
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val	
65 70 75 80	
Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn Thr	
85 90 95	
Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr Val	
100 105 110	
Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly	
115 120 125	
Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala	
130 135 140	
Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln	
145 150 155 160	
Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly	

165

170

175

His Arg Met Ala
180

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR36-9-20

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

C	GTC	GGC	GCT	CCC	GTA	GGA	GGC	GTC	GCA	AGA	GCC	CTT	GCG	CAT	GGC	46
Val	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly		
1					5					10				15		
GTG	AGG	GCC	CTT	GAA	GAC	GGG	ATA	AAT	TTC	GCA	ACA	GGG	AAT	TTG	CCC	94
Val	Arg	Ala	Leu	Glu	Asp	Gly	Ile	Asn	Phe	Ala	Thr	Gly	Asn	Leu	Pro	
				20					25					30		
GGT	TGC	TCC	TTT	TCT	ATT	TTC	CTT	CTT	GCT	CTG	TTC	TCT	TGC	TTA	ATT	142
Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Phe	Ser	Cys	Leu	Ile	
			35					40					45			
CAT	CCA	GCA	GCT	AGT	CTA	GAG	TGG	CGG	AAT	ACG	TCT	GGC	CTC	TAT	GTC	190
His	Pro	Ala	Ala	Ser	Leu	Glu	Trp	Arg	Asn	Thr	Ser	Gly	Leu	Tyr	Val	
			50				55					60				
CTT	ACC	AAC	GAC	TGT	TCC	AAT	AGC	AGT	ATT	GTG	TAC	GAG	GCC	GAT	GAC	238
Leu	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asp	
	65					70					75					
GTT	ATT	CTG	CAC	ACA	CCC	GGC	TGC	ATA	CCT	TGT	GTC	CAG	GAC	GGC	AAT	286
Val	Ile	Leu	His	Thr	Pro	Gly	Cys	Ile	Pro	Cys	Val	Gln	Asp	Gly	Asn	
80					85				90					95		
ACA	TCC	ACG	TGC	TGG	ACC	CCA	GTG	ACA	CCT	ACA	GTG	GCA	GTC	AAG	TAC	334
Thr	Ser	Thr	Cys	Trp	Thr	Pro	Val	Thr	Pro	Thr	Val	Ala	Val	Lys	Tyr	
				100					105					110		

GTC GGA GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val	
115 120 125	
GGC GCG GCC ACG ATG TGC TCT GCG CTC TAC GTG GGT GAC ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	
GCT GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT	478
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	
145 150 155	
CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA	526
Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser	
160 165 170 175	
GGA CAT CGA ATG GCT	541
Gly His Arg Met Ala	
180	

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val	
1 5 10 15	
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly	
20 25 30	
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His	
35 40 45	
Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu	
50 55 60	
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val	
65 70 75 80	
Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn Thr	
85 90 95	
Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr Val	
100 105 110	
Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly	
115 120 125	
Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala	
130 135 140	

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
 165 170 175

His Arg Met Ala
 180

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR33-1-10

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGT AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC GCG CCC GGC TGT GTA CCT TGT GTC CAG GAC GGC AAT	286
Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	

ACG TCT ACA TGC TGG ACC CCA GTA ACA CCT ACA GTG GCA GTC AGG TAC	334
Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	
100 105 110	
GTC GGG GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTG TTA GTA	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val	
115 120 125	
GGC GCG GCC ACG ATG TGC TCT GCG CTT TAC GTG GGT GAT ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCC CGC CGC CAT	478
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	
145 150 155	
CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA	526
Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser	
160 165 170 175	
GGA CAT CGC ATG GCT	541
Gly His Arg Met Ala	
180	

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val	
1 5 10 15	
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly	
20 25 30	
Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His	
35 40 45	
Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu	
50 55 60	
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val	
65 70 75 80	
Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr	
85 90 95	
Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val	
100 105 110	
Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly	

115	120	125
Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala		
130	135	140
Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln		
145	150	155
		160
Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly		
	165	170
		175
His Arg Met Ala		
180		

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR33-1-19

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCT TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGT AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	

GTT ATT CTG CAC GCG CCC GGC TGT GTA CCT TGT GTC CAG GAC GGC AAT 286
 Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn
 80 85 90 95
 ACG TCT ACA TGC TGG ACC CCA GTA ACA CCT ACA GTG GCA GTC AGG TAC 334
 Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr
 100 105 110
 GTC GGG GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTG TTA GTA 382
 Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val
 115 120 125
 GGC GCG GCC ACG ATG TGC TCT GCG CTT TAC GTG GGT GAT ATG TGT GGG 430
 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly
 130 135 140
 GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCC CGC CGC CAT 478
 Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His
 145 150 155
 CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA 526
 Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser
 160 165 170 175
 GGA CAT CGA ATG GCT 541
 Gly His Arg Met Ala
 180

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val
 1 5 10 15
 Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly
 20 25 30
 Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His
 35 40 45
 Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
 50 55 60
 Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val
 65 70 75 80
 Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr
 85 90 95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
 100 105 110

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly
 115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala
 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
 165 170 175

His Arg Met Ala
 180

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BR33-1-20

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

C	GTC	GGC	GCT	CCC	GTA	GGA	GGC	GTC	GCA	AGA	GCC	CTT	GCG	CAT	GGC	46
Val	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly		
1					5				10				15			
GTG	AGG	GCC	CTT	GAG	GAC	GGG	ATA	AAC	TTC	GCA	ACA	GGG	AAT	TTG	CCC	94
Val	Arg	Ala	Leu	Glu	Asp	Gly	Ile	Asn	Phe	Ala	Thr	Gly	Asn	Leu	Pro	
			20					25					30			
GGT	TGC	TCT	TTT	TCT	ATC	TTC	CTT	CTT	GCT	CTG	TTC	TCT	TGC	TTA	ATC	142
Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Phe	Ser	Cys	Leu	Ile	
			35					40					45			
CAT	CCA	GCA	GCT	GGT	CTA	GAG	TGG	CGG	AAT	ACG	TCT	GGC	CTC	TAT	GTC	190
His	Pro	Ala	Ala	Gly	Leu	Glu	Trp	Arg	Asn	Thr	Ser	Gly	Leu	Tyr	Val	
			50					55					60			

CTT ACC AAC GAC TGT TCC AAT AGT AGT ATT GTG TAT GAG GCC GAT GAC 238
 Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp
 65 70 75

GTT ATT CTG CAC GCG CCC GGC TGT GTA CCT TGT GTC CAG GAC GGC AAT 286
 Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn
 80 85 90 95

ACG TCT ACA TGC TGG ACC CCA GTA ACA CCT ACA GTG GCA GTC AGG TAC 334
 Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr
 100 105 110

GTC GGG GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTG TTA GTA 382
 Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val
 115 120 125

GGC GCG GCC ACG ATG TGC TCT GCG CTT TAC GTG GGT GAT ATG TGT GGG 430
 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly
 130 135 140

GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCC CGC CGC CAT 478
 Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His
 145 150 155

CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA 526
 Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser
 160 165 170 175

GGA CAT CGA ATG GCT 541
 Gly His Arg Met Ala
 180

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val
 1 5 10 15
 Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly
 20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His
 35 40 45

Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
 50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val
 65 70 75 80

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Ser Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu
 50 55 60

CAT GGA CCT ACG CCT CTT CTA TAT CGG TTG GGG CCT GTC CAA AAT GAA 239
 His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu
 65 70 75

ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG GCA TGC ATG TCA 287
 Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser
 80 85 90 95

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His
 1 5 10 15

Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu Thr
 20 25 30

Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser
 35 40 45

Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu His
 50 55 60

Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile
 65 70 75 80

Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser
 85 90 95

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HD10-1-25

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC GTC ACA AAA TAC ATT ATG	47
Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met	
1 5 10 15	
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTG TTG	95
Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu	
20 25 30	
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGC	143
Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly	
35 40 45	
TGC GTT GTA ATC GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA CTC	191
Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu	
50 55 60	
GTT CCA GAC AAG GAG GTG TTG TAT CAA CAG TAC GAT GAG ATG GAG GAG	239
Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu	
65 70 75	
TGC TCG CAA GCC GCC CCA TAC ATC GAA CAA GCT CAG GTA ATA GCC CAC	287
Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His	
80 85 90 95	
CAG TTC AAG GAG AAA ATC CTT GGA CTG CTG CAG CGA GCC ACC CAA CAA	335
Gln Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln	
100 105 110	
CAA GCT GTC ATT GAG CCC GTA ATA GCT TCC AAC TGG CAA AAG CTT GAA	383
Gln Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu	
115 120 125	
ACC TTC TGG CAC AAG CAT	401
Thr Phe Trp His Lys His	
130	

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met Ala
1 5 10 15

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu
 20 25 30
 Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys
 35 40 45
 Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu Val
 50 55 60
 Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys
 65 70 75 80
 Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
 85 90 95
 Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln
 100 105 110
 Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu Thr
 115 120 125
 Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-1-3

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC GTC ACA AAA TAC ATT ATG	47
Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met	
1 5 10 15	
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTG TTG	95
Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu	
20 25 30	
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGC	143

Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly
 35 40 45
 TGC GTT GTA ATC GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA CTC 191
 Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu
 50 55 60
 GTT CCA GAC AAG GAG GTG TTG TAT CAA CAG TAC GAT GAG ATG GAG GAG 239
 Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu
 65 70 75
 TGC TCG CAA GCC GCC CCA TAC ATC GAA CAA GCT CAG GTA ATA GCC CAC 287
 Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His
 80 85 90 95
 CAG TTC AAG GAG AAA ATC CTT GGA CTG CTG CAG CGA GCC ACC CAA CAA 335
 Gln Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln
 100 105 110
 CAA GCT GTC ATT GAG CCC GTA ATA GCT TCC AAC TGG CAA AAG CTT GAA 383
 Gln Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu
 115 120 125
 ACC TTC TGG CAC AAG CAT 401
 Thr Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met Ala
 1 5 10 15
 Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu
 20 25 30
 Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys
 35 40 45
 Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu Val
 50 55 60
 Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys
 65 70 75 80
 Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
 85 90 95
 Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln

100

105

110

Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu Thr
 115 120 125

Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-20-164

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG	47
Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met	
1 5 10 15	
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG	95
Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu	
20 25 30	
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT	143
Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly	
35 40 45	
TGT GTT GTG ATT GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC	191
Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile	
50 55 60	
GTT CCA GAC AAA GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG	239
Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu	
65 70 75	
TGC TCA CAA GCT GCC CCA TAT ATC GAA CAA GCT CAG GTA ATA GCT CAC	287
Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His	
80 85 90 95	
CAG TTC AAG GGA AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA	335

Gln Phe Lys Gly Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln
 100 105 110

CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG 383
 Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu
 115 120 125

GCC TTT TGG CAC AAG CAT 401
 Ala Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala
 1 5 10 15
 Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu
 20 25 30
 Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys
 35 40 45
 Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val
 50 55 60
 Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys
 65 70 75 80
 Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
 85 90 95
 Phe Lys Gly Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln
 100 105 110
 Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala
 115 120 125
 Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: BR36-20-166

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG	47
Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met	
1 5 10 15	
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG	95
Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu	
20 25 30	
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT	143
Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly	
35 40 45	
TGT GTT GTG ATT GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC	191
Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile	
50 55 60	
GTT CCA GAC AAA GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG	239
Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu	
65 70 75	
TGC TCA CAA GCT GCC CCA TAT ATC GAA CAA GCT CAG GTG ATA GCT CAC	287
Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His	
80 85 90 95	
CAG TTC AAG GAA AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA	335
Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln	
100 105 110	
CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG	383
Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu	
115 120 125	
GCC TTT TGG CAC AAG CAT	401
Ala Phe Trp His Lys His	
130	

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala
 1 5 10 15
 Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu
 20 25 30
 Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys
 35 40 45
 Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val
 50 55 60
 Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys
 65 70 75 80
 Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
 85 90 95
 Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln
 100 105 110
 Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala
 115 120 125
 Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-20-165

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG 47
 Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met
 1 5 10 15

GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG 95
 Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu
 20 25 30

CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT 143
 Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly
 35 40 45

TGT GTT GTG ATT GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC 191
 Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile
 50 55 60

GTT CCA GAC AAA GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG 239
 Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu
 65 70 75

TGC TCA CAA GCT GCC CCA TAT ATC GAA CAA GCT CAG GTA ATA GCT CAC 287
 Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His
 80 85 90 95

CAG TTC AAG GAA AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA 335
 Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln
 100 105 110

CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG 383
 Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu
 115 120 125

GCC TTT TGG CAC AAG CAT 401
 Ala Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala
 1 5 10 15

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu
 20 25 30

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys
 35 40 45

Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val
 50 55 60

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys
 65 70 75 80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
 85 90 95

Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln
 100 105 110

Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala
 115 120 125

Phe Trp His Lys His
 130

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-2-1

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val	
20 25 30	
GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC	143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	
35 40 45	
GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	

50	55	60	
CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC			239
Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro			
65	70	75	
GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG			287
Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly			
80	85	90	95
TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC			335
Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp			
100	105	110	
CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG			383
Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr			
115	120	125	
TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC			431
Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro			
130	135	140	
ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG			479
Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu			
145	150	155	
GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA			509
Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu			
160	165		

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala	
35 40 45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly	
65 70 75 80	
Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp	

85

90

95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110

Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile
 130 135 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160

Gly Val Asn Tyr Ala Thr Gly Asn Leu
 165

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-2-6

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val	
20 25 30	
GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC	143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	
35 40 45	
GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	
50 55 60	

CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC 239
 Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro
 65 70 75
 GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG 287
 Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly
 80 85 90 95
 TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC 335
 Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp
 100 105 110
 CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG 383
 Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr
 115 120 125
 TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC 431
 Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro
 130 135 140
 ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG 479
 Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu
 145 150 155
 GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA 509
 Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu
 160 165

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15
 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala
 35 40 45
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60
 Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly
 65 70 75 80
 Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile
 130 135 140
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160
 Gly Val Asn Tyr Ala Thr Gly Asn Leu
 165

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-4-1

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

A	ACG	TGC	GGA	TTC	GCC	GAT	CTC	ATG	GGG	TAT	ATC	CCG	CTC	GTA	GGC	46
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	
	1				5					10					15	
GGC	CCC	ATT	GGG	GGC	GTC	GCA	AGG	GCT	CTC	GCA	CAC	GGT	GTG	AGG	GTC	94
Gly	Pro	Ile	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	
			20					25					30			
CTT	GAG	GAC	GGG	GTA	AAC	TAT	GCA	ACA	GGG	AAT	TTA	CCC	GGT	TGC	TCT	142
Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	
			35				40						45			
TTC	TCT	ATC	TTT	ATT	CTT	GCT	CTT	CTC	TCG	TGT	CTG	ACC	GTT	CCG	GCC	190
Phe	Ser	Ile	Phe	Ile	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	
			50				55					60				
TCT	GCA	GTT	CCC	TAC	CGA	AAT	GCC	TCT	GGG	ATT	TAT	CAT	GTT	ACC	AAT	238

Ser	Ala	Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	
65						70					75					
GAT	TGC	CCA	AAC	TCT	TCC	ATA	GTC	TAT	GAG	GCA	GAT	AAC	CTG	ATC	CTA	286
Asp	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asn	Leu	Ile	Leu	
80					85				90						95	
CAC	GCA	CCT	GGT	TGC	GTG	CCT	TGT	GTC	ATG	ACA	GGT	AAT	GTG	AGT	AGA	334
His	Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Met	Thr	Gly	Asn	Val	Ser	Arg	
				100					105					110		
TGC	TGG	GTC	CAA	ATT	ACC	CCT	ACA	CTG	TCA	GCC	CCG	AGC	CTC	GGA	GCA	382
Cys	Trp	Val	Gln	Ile	Thr	Pro	Thr	Leu	Ser	Ala	Pro	Ser	Leu	Gly	Ala	
			115					120					125			
GTC	ACG	GCT	CCT	CTT	CGG	AGA	GCC	GTT	GAC	TAC	CTA	GCG	GGA	GGG	GCT	430
Val	Thr	Ala	Pro	Leu	Arg	Arg	Ala	Val	Asp	Tyr	Leu	Ala	Gly	Gly	Ala	
			130				135					140				
GCC	CTC	TGC	TCC	GCG	TTA	TAC	GTA	GGA	GAC	GCG	TGT	GGG	GCA	CTA	TTC	478
Ala	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Ala	Cys	Gly	Ala	Leu	Phe	
		145				150					155					
TTG	GTA	GGC	CAA	ATG	TTC	ACC	TAT	AGG	CCT	CGC	CAG	CAC	GCT	ACG	GTG	526
Leu	Val	Gly	Gln	Met	Phe	Thr	Tyr	Arg	Pro	Arg	Gln	His	Ala	Thr	Val	
160					165				170						175	
CAG	AAC	TGC	AAC	TGT	TCC	ATT	TAC	AGT	GGC	CAT	GTT	ACC	GGC	CAC	CGG	574
Gln	Asn	Cys	Asn	Cys	Ser	Ile	Tyr	Ser	Gly	His	Val	Thr	Gly	His	Arg	
				180					185					190		
ATG	GCA															580
Met	Ala															

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Gly	
1				5				10						15		
Pro	Ile	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	
			20					25					30			
Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	
		35				40					45					
Ser	Ile	Phe	Ile	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	
	50					55					60					

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His
85 90 95

Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys
100 105 110

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val
115 120 125

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala
130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
165 170 175

Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-4-6

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

A ACG TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC 46
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly
1 5 10 15

GGC CCC ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC 94

(2) INFORMATION FOR SEQ ID NO: 48:

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly
 1 5 10 15
 Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
 20 25 30
 Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45
 Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
 50 55 60
 Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
 65 70 75 80
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His
 85 90 95
 Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys
 100 105 110
 Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val
 115 120 125
 Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala
 130 135 140
 Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
 145 150 155 160
 Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
 165 170 175
 Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met
 180 185 190
 Ala

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 959 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: PC-3-4

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val	
20 25 30	
GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC	143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	
35 40 45	
GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	
50 55 60	
CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC	239
Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro	
65 70 75	
GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG	287
Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly	
80 85 90 95	
TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC	335
Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp	
100 105 110	
CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG	383
Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr	
115 120 125	
TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC	431
Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro	
130 135 140	
ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG	479
Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu	
145 150 155	
GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA CCC GGT TGC TCT TTC TCT	527
Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser	
160 165 170 175	
ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC TCT GCA	575
Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala	
180 185 190	
GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT GAT TGC	623
Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys	
195 200 205	

CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA CAC GCA 671
 Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala
 210 215 220

CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA TGC TGG 719
 Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp
 225 230 235

GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA GTC ACG 767
 Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr
 240 245 250 255

GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT GCC CTC 815
 Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu
 260 265 270

TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC TTG GTA 863
 Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val
 275 280 285

GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG CAG AAC 911
 Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn
 290 295 300

TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG ATG GCA 959
 Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala
 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60

Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly
 65 70 75 80

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile
 130 135 140
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160
 Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
 165 170 175
 Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val
 180 185 190
 Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro
 195 200 205
 Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro
 210 215 220
 Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val
 225 230 235 240
 Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala
 245 250 255
 Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys
 260 265 270
 Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly
 275 280 285
 Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys
 290 295 300
 Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 959 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-3-8

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val	
20 25 30	
GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC	143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	
35 40 45	
GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	
50 55 60	
CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC	239
Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro	
65 70 75	
GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG	287
Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly	
80 85 90 95	
TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC	335
Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp	
100 105 110	
CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG	383
Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr	
115 120 125	
TGC GGA TTC GCC GAT CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC	431
Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro	
130 135 140	
GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG	479
Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu	
145 150 155	
GAC GGG GTA AAC TAT CCA ACA GGG AAT TTA CCC GGT TGC TCT TTC TCT	527
Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser	
160 165 170 175	
ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC TCT GCA	575
Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala	
180 185 190	
GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT GAT TGC	623

Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys
 195 200 205

CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA CAC GCA 671
 Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala
 210 215 220

CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA TGC TGG 719
 Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp
 225 230 235

GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA GTC ACG 767
 Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr
 240 245 250 255

GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT GCC CTC 815
 Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu
 260 265 270

TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC TTG GTA 863
 Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val
 275 280 285

GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG CAG AAC 911
 Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn
 290 295 300

TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG ATG GCA 959
 Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala
 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60

Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly
 65 70 75 80

Tyr	Pro	Trp	Pro	Leu	Tyr	Ala	Asn	Glu	Gly	Leu	Gly	Trp	Ala	Gly	Trp	
				85					90					95		
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Asn	Trp	Gly	Pro	Asn	Asp	Pro	
				100					105					110		
Arg	Arg	Lys	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	
				115					120					125		
Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Gly	Pro	Val	
				130					135					140		
Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	
145					150					155					160	
Gly	Val	Asn	Tyr	Pro	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	
				165					170					175		
Phe	Ile	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Val	
				180					185					190		
Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp	Cys	Pro	
				195					200					205		
Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asn	Leu	Ile	Leu	His	Ala	Pro	
				210					215					220		
Gly	Cys	Val	Pro	Cys	Val	Met	Thr	Gly	Asn	Val	Ser	Arg	Cys	Trp	Val	
225					230					235					240	
Gln	Ile	Thr	Pro	Thr	Leu	Ser	Ala	Pro	Ser	Leu	Gly	Ala	Val	Thr	Ala	
				245					250					255		
Pro	Leu	Arg	Arg	Ala	Val	Asp	Tyr	Leu	Ala	Gly	Gly	Ala	Ala	Leu	Cys	
				260					265					270		
Ser	Ala	Leu	Tyr	Val	Gly	Asp	Ala	Cys	Gly	Ala	Leu	Phe	Leu	Val	Gly	
				275					280					285		
Gln	Met	Phe	Thr	Tyr	Arg	Pro	Arg	Gln	His	Ala	Thr	Val	Gln	Asn	Cys	
				290					295					300		
Asn	Cys	Ser	Ile	Tyr	Ser	Gly	His	Val	Thr	Gly	His	Arg	Met	Ala		
305					310					315						

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 959 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

[illegible]

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC C/E1

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

CCATGAGCAC GAATCCTAAA CCTCAAAGAA AAACCAAAAG AAACACCAAC CGTCGCCCAC	60
AGGACGTCAA GTTCCCGGGC GGTGGTCAGA TCGTTGGCGG AGTTTACTTG TTGCCGCGCA	120
GGGGCCCTAG GATGGGTGTG CGCGCGACTC GGAAGACTTC GGAACGGTCG CAACCCCGTG	180
GACGGCGTCA GCCTATTCCC AAGGCGCGCC AGCCACGGG CCGGTCCTGG GGTCAACCCG	240
GGTACCCTTG GCCCCTTTAC GCCAATGAGG GCCTCGGGTG GGCAGGGTGG CTGCTCTCCC	300
CTCGAGGCTC TCGGCCTAAT TGGGGCCCCA ATGACCCCCG GCGAAAATCG CGTAATTTGG	360
GTAAGGTCAT CGATACCCTA ACGTGCGGAT TCGCCGATCT CATGGGGTAY ATCCCGCTCG	420
TAGGCGGCCC CRTTGGGGGC GTCGCAAGGG CTCTCGCACA CGGTGTGAGG GTCCTTGAGG	480
ACGGGGTAAA CTATSCAACA GGGAATTTAC CCGGTTGCTC TTTCTCTATC TTTATTCTTG	540
CTCTTCTCTC GTGTCTGACC GTTCCGGCCT CTGCAGTTCC CTACCGAAAT GCCTCTGGGA	600
TTTATCATGT TACCAATGAT TGCCCAAACCT CTTCATAGT CTATGAGGCA GATAACCTGA	660
TCCTACACGC ACCTGGTTGC GTGCCTTGTG TCATGACAGG TAATGTGAGT AGATGCTGGG	720
TCCAAATTAC CCCTACACTG TCAGCCCCGA GCCTCGGAGC AGTCACGGCT CCTCTTCGGA	780
GAGCCGTTGA CTACCTAGCG GGAGGGGCTG CCCTCTGCTC CGCGTTATAC GTAGGAGACG	840
CGTGTGGGGC ACTATTCTTG GTAGGCCAAA TGTTACCTA TAGGCCTCGC CAGCACGCTA	900
CGGTGCAGAA CTGCAACTGT TCCATTTACA GTGGCCATGT TACCGGCCAC CGGATGGCA	959

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5					10					15	

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala
 35 40 45
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60
 Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly
 65 70 75 80
 Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Val
 130 135 140
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160
 Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
 165 170 175
 Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val
 180 185 190
 Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro
 195 200 205
 Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro
 210 215 220
 Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val
 225 230 235 240
 Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala
 245 250 255
 Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys
 260 265 270
 Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly
 275 280 285
 Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys
 290 295 300
 Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-1-37

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

ACCACCGGAG CTTCTATCAC ATACTCCACT TACGGCAAGT TCCTTGCTGA TGGAGGGTGT      60
TCAGGCGGCG CGCATGACGT GATCATATGC GACGAGTGCC ATTCCCAGGA CGCCACCACC      120
ATTCTTGGGA TAGGCACTGT CCTTGACCAG GCAGAGACGG CTGGAGCTAG GCTCGTCGTC      180
TTGGCCACGG NCACCCCTCC CGGCAGTGTG ACAACGCCCC ACCCCAACAT CGAGGAAGTG      240
GCCCTGCCTC AGGAGGGGGA GGTTCCTTC TACGGCAGAG CCATTCCCCT TGCTTTTATA      300
AAGGGTGGTA GGCATCTCAT CTTCTGCCAT TCCAAGAAAA ATTGTGATGA ACTC          354

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(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala
1           5           10           15

Asp Gly Gly Cys Ser Gly Gly Ala His Asp Val Ile Ile Cys Asp Glu
          20           25           30

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Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr Val Leu
 35 40 45
 Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Xaa
 50 55 60
 Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu Glu Val
 65 70 75 80
 Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala Ile Pro
 85 90 95
 Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys
 100 105 110
 Lys Asn Cys Asp Glu Leu
 115

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-1-48

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ACCACCGGAG CTTCTATCAC ATACTCCACT TACGGCAAGT TCCTTGCTGA TGGAGGGTGT 60
 TCAGGCGGCG CGTATGACGT GATCATATGC GACGAGTGCC ATTCCCAGGA CGCCACCACC 120
 ATTCTTGGGA TAGGCACTGT CCTTGACCAG GCAGAGACGG CTGGAGCTAG GCTCGTCGTC 180
 TTGGNCACGG NCACCCCTCC CGGCAGTGTG ACAACGCCCC ACCCCAACAT CGAGGAAGTG 240
 GCCCTGCCTC AGGAGGGGGA GGTTCCTTC TACGGNAGAG CCATTCCCCT TGCTTTTATA 300
 AAGGGTGGTA GGCATCTCAT CTTCTGCCAT TCCAAGAAAA AATGTGATGA ACTT 354

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala
1           5           10           15
Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys Asp Glu
          20          25          30
Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr Val Leu
          35          40          45
Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Xaa Thr Xaa
          50          55          60
Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu Glu Val
65          70          75          80
Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Xaa Arg Ala Ile Pro
          85          90          95
Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys
          100          105          110
Lys Lys Cys Asp Glu Leu Arg Gln Ala Thr Asp Gln Pro Gly Arg Glu
          115          120          125
Arg Pro Trp Glu Tyr
          130

```

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-1-37

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

ATGGCTTTCA TGTCTCCGGA CTGGAGGTC ATTACCANCA CTGGGTTCT GGTGGGGGGC      60
GTTGTGGCGA CCCTGNCGNC CTACTGCTTG ACGGTGGGTT CGGTAGCCAT AGTCGGTAGG      120
ATCATCCTCT CTGGGAAACC TGCCATCATT NCCGATAGGG AGGTATTATA CCAGCAATTT      180
GATGAGATGG AGGAGTGCTC GGCCTCGTTG CCCTATATGG ACGAAACACG TNCCATTGCC      240
GGACAATTCA AAGAGAAAGT GCTCGGCTTC ATGACACGA CCGGCCAGAA GGCTGAAACT      300
CTGAAGCCGG CAGCCACGTC TGTGTGGAAC AAGGCTGATC AGTTCTGGNC CACATAC      357

```

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```

Met Ala Phe Met Ser Pro Asp Leu Glu Val Ile Thr Xaa Thr Trp Val
1           5           10           15
Leu Val Gly Gly Val Val Ala Thr Leu Xaa Xaa Tyr Cys Leu Thr Val
20           25           30
Gly Ser Val Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala
35           40           45
Ile Ile Xaa Asp Arg Glu Val Leu Tyr Gln Gln Phe Asp Glu Met Glu
50           55           60
Glu Cys Ser Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Xaa Ile Ala
65           70           75           80
Gly Gln Phe Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln
85           90           95
Lys Ala Glu Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala
100          105          110
Asp Gln Phe Trp Xaa Thr Tyr Met Trp Asn Phe Ile Ser Gly Ile Gln
115          120          125

```

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

Glu	Cys	Ser	Ala	Ser	Leu	Pro	Tyr	Met	Asp	Glu	Thr	Arg	Ala	Ile	Ala
65					70					75				80	
Gly	Gln	Phe	Lys	Glu	Lys	Val	Leu	Gly	Phe	Ile	Ser	Thr	Thr	Gly	Gln
				85					90					95	
Lys	Ala	Glu	Thr	Leu	Lys	Pro	Ala	Ala	Thr	Ser	Val	Trp	Asn	Lys	Ala
				100				105					110		
Xaa	Gln	Phe	Trp	Ala	Thr	Tyr	Met	Trp	Asn	Phe	Ile	Ser	Gly	Ile	Gln
				115			120					125			

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCP161"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ACCGGAGGCC AGGAGAGTGA TCTCCTCC

28

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCP162"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GGGCTGCTCT ATCCTCATCG ACGCCATC

28

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPrl63"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GCCAGAGGCT CGGAAGGCGA TCAGCGCT

28

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPrl64"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GAGCTGCTCT GTCCTCCTCG ACGCCGCA

28

(2) INFORMATION FOR SEQ ID NO: 67:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..28
 (D) OTHER INFORMATION: /standard_name= "HCV Primer
 HCPPr23"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

CTCATGGGGT ACATTCCGCT

20

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: YES
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..28
 (D) OTHER INFORMATION: /standard_name= "HCV Primer
 HCPPr54"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

CTATTACCAG TTCATCATCA TATCCCA

27

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPrl16"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

TTTTAAATAC ATCATGRCTG YATG

24

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCP66"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CTATTATTGT ATCCCRCTGA TGAARTTCCA CAT

33

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..28
(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPrl18:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ACTAGTCGAC TAYTGATCCR CTATRWARTT CCACAT

36

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..28
(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPrl17:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

TTTTAAATAC ATCGCRCTGC ATGCA

25

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..28
(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPrl19:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

ACTAGTCGAC TARTTGCATA GCCKRTTCAT CCAYTG

36

(2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPri131:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

GGAATTCTAG ACCTCTGGGA YGARAYTGGA ARTG

34

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPri130:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GGAATTCTAG ACGCTAYCAR GCACGTTGYG C

31

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPri134:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CATATAGATG CCCACTTCCT ATC

23

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPri3:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GTGTGCCAGG ACCATC

16

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCP4:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

GACATGCATG TCATGATGTA

20

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard_name= "HCV Primer
HCP152:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TACGCCTCTT CTATATCGGT TGGGGCCTG

29

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPPr52:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

ATGTTGGGTA AGGTCATCGA TACCCT

26

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPPr41:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CCCGGGAGGT CTCGTAGACC GTGCA

25

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer
HCPPr40:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CTATTAAAGA TAGAGAAAGA GCAACCGGG

29

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 192 to 203 of the V1 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 192 to 203 of the V1 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 213 to 223 of the V2 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Val	Tyr	Glu	Ala	Asp	Asp	Val	Ile	Leu	His	Thr
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 213 to 233 of the V2 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Val	Tyr	Glu	Ala	Asp	Asn	Leu	Ile	Leu	His	Ala
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 242 of the V3 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Val Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 242 of the V3 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Val Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 248 to 257 of the V4 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Val Arg Tyr Val Gly Ala Thr Thr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 248 to 257 of the V4 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Ala	Pro	Ser	Leu	Gly	Ala	Val	Thr	Ala	Pro
1				5				10	

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 294 to 303 of the V5 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Arg	Pro	Arg	Arg	His	Gln	Thr	Val	Gln	Thr
1				5				10	

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 294 to 303 of the V5 region of HCV
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Arg Pro Arg Gln His Ala Thr Val Gln Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 70 to 78 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Gln Pro Thr Gly Arg Ser Trp Gly Gln
1 5

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR33 and BR36

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 237 of the V3 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

Val Gln Asp Gly Asn Thr Ser Thr
1 5

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HD10

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 237 of the V3 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

Val Gln Asp Gly Asn Thr Ser Ala
1 5

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR36

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 248 to 257 of the V4 region of HCV
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

Val Lys Tyr Val Gly Ala Thr Thr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR36

(viii) POSITION IN GENOME:

(B) MAP POSITION: Positions 1688 to 1707 of HCV type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys Glu Val Leu Tyr Gln
1 5 10 15
Gln Tyr Asp Glu
 20

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HD10

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1688 to 1707 of HCV type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

Leu Gly Gly Lys Pro Ala Leu Val Pro Asp Lys Glu Val Leu Tyr Gln
1 5 10 15
Gln Tyr Asp Glu
 20

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1712 to 1731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln
 1 5 10 15

Phe Lys Glu Lys
 20

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR36

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1724 to 1743 of HCV type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

Ile Ala His Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala
 1 5 10 15

Thr Gln Gln Gln
 20

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HD10

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1724 to 1743 of HCV type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

Ile Ala His Gln Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala
 1 5 10 15

Thr Gln Gln Gln
20

(2) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1688 to 1707 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Ala Leu Tyr Gln
1 5 10 15

Gln Phe Asp Glu
20

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1688 to 1707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val Leu Tyr Gln
1 5 10 15

Gln Phe Asp Glu
20

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: position 1712 to 1731 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

Ser	Ala	Ser	Leu	Pro	Tyr	Met	Asp	Glu	Thr	Arg	Ala	Ile	Ala	Gly	Gln
1				5					10					15	
Phe	Lys	Glu	Lys												
				20											

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1724 to 1743 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

Ile	Ala	Gly	Gln	Phe	Lys	Glu	Lys	Val	Leu	Gly	Phe	Ile	Ser	Thr	Thr
1				5				10					15		
Gly	Gln	Lys	Ala												
				20											

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB48-3-10

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GAG GTC TAT	46
Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAC CTG GAG CCC GAA GCC CGC AAG GCA ATT ACC GCC CTA	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala Leu	
20 25 30	
ACA GAG AGA CTC TAC GTG GGC GGT CCC ATG CAT AAC AGC AAG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp	
35 40 45	
CTG TGC GGG TAT CGC AGA TGT CGC GCA AGC GGC GTC TAC ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACA CTG ACG TGC TAC CTC AAA GCC TCA GCC GCT ATC AAA	238
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Lys	
65 70 75	
GCG GCG GGG CTG AGA GAC TGC ACC ATG TTG GTC TGT GGT GAT GAC CTG	286
Ala Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTT GTC ATC GCT GAG AGC GAT GGC GTA GAG GAG GAC AAA CGA CCC CTC	334
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Pro Leu	
100 105 110	
GGA GCC	340
Gly Ala	

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
1 5 10 15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB215-3-8

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

C TCC ACT GTA ACC GAA AAA GAC ATC AGG GTC GAG GAG GAG GTA TAT	46
Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAC CTG GAG CCC GAA GCC CGC AAG GTA ATT ACC GCC CTA	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu	
20 25 30	
ACA GAG AGA CTC TAT GTG GGC GGT CCC ATG CAT AAT AGC AAA GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp	
35 40 45	
CTG TGC GGG TAT CGC AGA TGC CGC GCA AGC GGC GTC TAC ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACA CTG ACG TGC TAT CTC AAA GCC TCA GCC GCC ATC AGG	238
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg	
65 70 75	
GCG TCA GGG CTG AGA GAC TGC ACT ATG CTG GTC TAT GGT GAC GAC CTG	286
Ala Ser Gly Leu Arg Asp Cys Thr Met Leu Val Tyr Gly Asp Asp Leu	
80 85 90 95	
GTC GTC ATT GCC GAG AGC GAT GGC GTA GAG GAG GAC AAA CGA GCC CTC	334
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu	
100 105 110	
GGA GTC	340
Gly Val	

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
 1             5             10             15
Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr
          20             25             30
Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
          35             40             45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
          50             55             60
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
          65             70             75             80
Ser Gly Leu Arg Asp Cys Thr Met Leu Val Tyr Gly Asp Asp Leu Val
          85             90             95
Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
          100            105            110
Val

```

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB358-3-3

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GAG GTG TAT

46

Ala

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr
 1 5 10 15

CAG TGT TGT GAC CTG GAG CCC GAG GCC CGC AAG GCA ATT ACT GCC CTA 94
 Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala Leu
 20 25 30

ACA GAG AGA CTC TAT GTG GGC GGT CCC ATG CAT AAC AGC AAG GGA GAC 142
 Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp
 35 40 45

CTG TGT GGG TAT CGC AGA TGC CGC GCA AGC GGC GTC TAC ACC ACC AGC 190
 Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser
 50 55 60

TTC GGG AAC ACA CTG ACG TGC TAC CTC AAA GCC TCA GCC GCT ATC AGA 238
 Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg
 65 70 75

GCG GCG GGG CTG AGA GAC TGC ACC ATG TTG GTC TGT GGT GAT GAC CTG 286
 Ala Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu
 80 85 90 95

GTC GTC ATC GCT GAG AGC GAT GGC GTT GAG GAG GAC AAA CGA GCC CTC 334
 Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu
 100 105 110

GGA GCC 340
 Gly Ala

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
 1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala Leu Thr
 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
 50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
 65 70 75 80

GTC GTC ATC TGC GAG AGC GGC GGC GTA GAG GAG GAT GCA AGA GCC CTC 334
 Val Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu
 100 105 110

CGA GCC 340
 Arg Ala

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr Gln
 1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr
 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu
 35 40 45

Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
 50 55 60

Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg Ala
 65 70 75 80

Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95

Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: GB809-3-1

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

C TCC ACT GTG ACT GAG AGA GAC ATC AAG GTC GAA GAA GAA GTC TAT	46
Ser Thr Val Thr Glu Arg Asp Ile Lys Val Glu Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAT CTG GAG CCC GAG GCC CGC AAG GTA ATA GCC GCC CTC	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ala Ala Leu	
20 25 30	
ACG GAG AGA CTC TAC GTG GGC GGC CCC ATG CAT AAC AGC AAG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp	
35 40 45	
CTT TGC GGG TAT CGT AGA TGC CGC GCG AGC GGC GTA TAC ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACA ATG ACG TGC TAC CTT AAG GCC TCA GCA GCC ATC AGG	238
Phe Gly Asn Thr Met Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg	
65 70 75	
GCT GCG GGG CTA AAG GAT TGC ACC ATG CTG GTT TGC GGT GAC GAC CTA	286
Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTC GTG ATC GCC GAG AGC GGT GGC GTT GAG GAG GAC AAA CGA GCC CTC	334
Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu	
100 105 110	
GGA GCT	
Gly Ala	340

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

Ser Thr Val Thr Glu Arg Asp Ile Lys Val Glu Glu Glu Val Tyr Gln
1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ala Ala Leu Thr
 20 25 30
 Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
 35 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
 50 55 60
 Gly Asn Thr Met Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
 65 70 75 80
 Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GB358-4-1

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC CTG GCA CAC GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGG ATC AAT TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	

TCT ATC TTC CTC TTG GCA CTT CTT TCG TGC CTG ACT GTT CCC ACC TCG 192
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser
 50 55 60

GCC GTC AAC TAT CGC AAT GCC TCG GGC ATC TAT CAC ATC ACC AAT GAC 240
 Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
 65 70 75 80

TGC CCG AAC TCG AGC ATA GTG TAC GAG ACC GAG CAC CAC ATC CTA CAC 288
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His
 85 90 95

CTC CCA GGG TGT TTA CCC TGC GTG AGG GTT GGG AAT CAG TCA CGC TGC 336
 Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys
 100 105 110

TGG GTG GCC CTC ACT CCC ACC GTG GCG GCG CCT TAC ATC GGC GCT CCG 384
 Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro
 115 120 125

CTT GAA TCC CTC CGG AGT CAT GTG GAT CTG ATG GTA GGT GCC GCT ACT 432
 Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140

GCG TGC TCC GCT CTT TAC ATC GGA GAC CTG TGC GGT GGC GTA TTC TTG 480
 Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
 145 150 155 160

GTT GGT CAG ATG TTC TCT TTC CAG CCG CGG CGC CAC TGG ACT ACG CAG 528
 Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln
 165 170 175

GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC GTT ACG GGC CAC AGG A 574
 Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg
 180 185 190

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser

50	55	60
Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp		
65	70	75 80
Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His		
	85	90 95
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys		
	100	105 110
Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro		
	115	120 125
Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr		
	130	135 140
Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu		
145	150	155 160
Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln		
	165	170 175
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg		
	180	185 190

(2) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: GB549-4-3
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

ACG TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC TTG GCA CAT GGT GTC AGG GCC GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	

GAG GAC GGG ATT AAC TAT GCA ACA GGG AAT CTT CCC GGT TGC TCC TTT 144
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45
 TCT ATC TTC CTT CTA GCA CTT CTC TCG TGC TTG ACT GTC CCG GCC TCG 192
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
 50 55 60
 GCG CAG CAC TAC CGG AAC ATC TCG GGC ATT TAT CAC GTC ACC AAT GAC 240
 Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp
 65 70 75 80
 TGC CCG AAC TCT AGT ATA GTG TAT GAA GCT GAC CAT CAT ATC ATG CAT 288
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His
 85 90 95
 CTA CCA GGG TGT GTG CCT TGC GTG AGA ACC GGG AAC ACC TCG CGC TGC 336
 Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys
 100 105 110
 TGG GTT CCT TTA ACA CCC ACT GTG GCT GCC CCC TAT GTT GGC GCG CCG 384
 Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro
 115 120 125
 CTC GAA TCC ATG CGG CGG CAC GTG GAC TTA ATG GTG GGT GCC GCC ACC 432
 Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140
 GTC TGC TCG GCC CTG TAC ATC GGA GAC CTT TGC GGA GGT GTC TTC CTG 480
 Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu
 145 150 155 160
 GTC GGG CAG ATG TTC ACC TTC CGG CCG CGC CGC CAT TGG ACT ACC CAG 528
 Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln
 165 170 175
 GAC TGC AAC TGC TCT ATC TAT GAT GGC CAC ATC ACC GGC CAT AGA A 574
 Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg
 180 185 190

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
 20 25 30

Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe
		35					40					45			
Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser
50						55					60				
Ala	Gln	His	Tyr	Arg	Asn	Ile	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp
65					70					75					80
Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	His	His	Ile	Met	His
				85					90					95	
Leu	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Thr	Gly	Asn	Thr	Ser	Arg	Cys
		100						105					110		
Trp	Val	Pro	Leu	Thr	Pro	Thr	Val	Ala	Ala	Pro	Tyr	Val	Gly	Ala	Pro
115						120						125			
Leu	Glu	Ser	Met	Arg	Arg	His	Val	Asp	Leu	Met	Val	Gly	Ala	Ala	Thr
130						135					140				
Val	Cys	Ser	Ala	Leu	Tyr	Ile	Gly	Asp	Leu	Cys	Gly	Gly	Val	Phe	Leu
145					150				155						160
Val	Gly	Gln	Met	Phe	Thr	Phe	Arg	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln
				165					170				175		
Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Asp	Gly	His	Ile	Thr	Gly	His	Arg	
		180						185				190			

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GB809-4-3

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

ACG TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC

Country	Year	Population (millions)	Urban population (millions)	Urban population (%)	Population density (per sq km)	Urban population density (per sq km)	Population growth rate (%)	Urban population growth rate (%)	Population growth rate (%)	Urban population growth rate (%)	Population growth rate (%)	Urban population growth rate (%)
Algeria	1980	10.0	4.0	40.0	100	250	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	1985	10.5	4.5	42.9	105	260	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	1990	11.0	5.0	45.5	110	270	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	1995	11.5	5.5	47.8	115	280	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2000	12.0	6.0	50.0	120	290	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2005	12.5	6.5	52.0	125	300	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2010	13.0	7.0	53.8	130	310	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2015	13.5	7.5	55.6	135	320	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2020	14.0	8.0	57.1	140	330	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2025	14.5	8.5	58.6	145	340	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2030	15.0	9.0	60.0	150	350	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2035	15.5	9.5	61.3	155	360	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2040	16.0	10.0	62.5	160	370	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2045	16.5	10.5	63.6	165	380	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2050	17.0	11.0	64.7	170	390	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2055	17.5	11.5	65.7	175	400	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2060	18.0	12.0	66.7	180	410	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2065	18.5	12.5	67.6	185	420	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2070	19.0	13.0	68.4	190	430	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2075	19.5	13.5	69.2	195	440	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2080	20.0	14.0	70.0	200	450	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2085	20.5	14.5	70.7	205	460	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2090	21.0	15.0	71.4	210	470	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2095	21.5	15.5	72.1	215	480	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2100	22.0	16.0	72.7	220	490	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2105	22.5	16.5	73.3	225	500	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2110	23.0	17.0	73.9	230	510	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2115	23.5	17.5	74.5	235	520	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2120	24.0	18.0	75.0	240	530	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2125	24.5	18.5	75.5	245	540	1.5	2.5	1.5	2.5	1.5	2.5
Algeria	2130	25.0	19.0	76.0	250	550	1.5	2.5	1.5	2.5	1.5	

Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	
1				5					10					15		
CCC	GTT	GGG	GGC	GTC	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	AGG	GCT	GTG	96
Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Ala	Val	
			20					25					30			
GAG	GAC	GGG	ATT	AAC	TAT	GCG	ACA	GGG	AAT	CTT	CCC	GGT	TGC	TCT	TTC	144
Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	
		35					40					45				
TCT	ATC	TTC	CTC	CTG	GCA	CTT	CTT	TCG	TGC	CTC	ACT	GTC	CCA	GCG	TCA	192
Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	
		50				55					60					
GCT	GAG	CAC	TAC	CGG	AAT	GCT	TCG	GGC	ATC	TAT	CAC	ATC	ACC	AAT	GAC	240
Ala	Glu	His	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Ile	Thr	Asn	Asp	
		65			70				75					80		
TGT	CCG	AAT	TCC	AGC	GTA	GTC	TAT	GAA	ACT	GAC	CAC	CAT	ATA	TTG	CAC	288
Cys	Pro	Asn	Ser	Ser	Val	Val	Tyr	Glu	Thr	Asp	His	His	Ile	Leu	His	
				85					90					95		
TTG	CCG	GGG	TGC	GTA	CCC	TGC	GTG	AGG	GCC	GGG	AAC	GTG	TCT	CGT	TGC	336
Leu	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Ala	Gly	Asn	Val	Ser	Arg	Cys	
			100					105				110				
TGG	ACG	CCG	GTA	ACA	CCT	ACG	GTG	GCT	GCC	GTA	TCC	ATG	GAC	GCT	CCG	384
Trp	Thr	Pro	Val	Thr	Pro	Thr	Val	Ala	Ala	Val	Ser	Met	Asp	Ala	Pro	
		115					120					125				
CTC	GAG	TCC	TTC	CGG	CGG	CAT	GTG	GAC	CTA	ATG	GTA	GGT	GCG	GCC	ACC	432
Leu	Glu	Ser	Phe	Arg	Arg	His	Val	Asp	Leu	Met	Val	Gly	Ala	Ala	Thr	
		130				135					140					
GTG	TGT	TCT	GTC	CTC	TAT	GTT	GGA	GAC	CTC	TGT	GGA	GGT	GCT	TTC	CTA	480
Val	Cys	Ser	Val	Leu	Tyr	Val	Gly	Asp	Leu	Cys	Gly	Gly	Ala	Phe	Leu	
		145			150				155					160		
GTG	GGG	CAG	ATG	TTC	ACC	TTC	CAG	CCG	CGT	CGC	CAC	TGG	ACC	ACG	CAG	528
Val	Gly	Gln	Met	Phe	Thr	Phe	Gln	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	
			165					170					175			
GAT	TGT	AAT	TGC	TCC	ATC	TAT	ACT	GGC	CAT	ATC	ACC	GGC	CAC	AGG	A	574
Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Thr	Gly	His	Ile	Thr	Gly	His	Arg		
			180					185					190			

(2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

TGGGGATCCC GTATGATACC CGCTGCTTTG A

31

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HcPr207"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

GGCGGAATTC CTGGTCATAG CCTCCGTGAA

30

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
 20 25 30
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
 50 55 60
 Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
 65 70 75 80
 Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His
 85 90 95
 Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys
 100 105 110
 Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro
 115 120 125
 Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr
 130 135 140
 Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu
 145 150 155 160
 Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln
 165 170 175
 Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg
 180 185 190

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCP206"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Amino acid
- (C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Amino acid
- (C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Val Tyr Glu Thr Glu His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 130:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: amino acid
 (C) INDIVIDUAL ISOLATE: GB549
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:
- | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Glu | Ala | Asp | His | His | Ile | Met | His | Leu |
| 1 | | | | 5 | | | | | 10 | |

- (2) INFORMATION FOR SEQ ID NO: 131:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: amino acid
 (C) INDIVIDUAL ISOLATE: GB809
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:
- | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Glu | Thr | Asp | His | His | Ile | Leu | His | Leu |
| 1 | | | | 5 | | | | | 10 | |

- (2) INFORMATION FOR SEQ ID NO: 132:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: amino acid
 (C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Val Arg Val Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

Val Arg Thr Gly Asn Thr Ser Arg Cys Trp Val Pro Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

Val Arg Ala Gly Asn Val Ser Arg Cys Trp Thr Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: amino acid

(C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

Ala	Pro	Tyr	Ile	Gly	Ala	Pro	Leu	Glu	Ser
1				5					10

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: amino acid

(C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

Ala	Pro	Tyr	Val	Gly	Ala	Pro	Leu	Glu	Ser
1				5					10

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: amino acid

(C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Ala	Val	Ser	Met	Asp	Ala	Pro	Leu	Glu	Ser
1				5					10

(2) INFORMATION FOR SEQ ID NO: 138:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB358 and GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

Gln	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	Asp
1				5				10	

(2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: amino acid
(C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

Arg	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	Asp
1				5				10	

(2) INFORMATION FOR SEQ ID NO: 140:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..957

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACT AAC	48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGC CAG ATC GTT GGT	96
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTA TAC TTG TTG CCG CGC AGG GGC CCC CGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACG AGG AAA ACT TCC GAG CGG TCC CAG CCA CGT GGG AGG CGC CAG CCC	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAA GAT CGG CGC CCC ACT GGC AAG TCC TGG GGA AAA CCA GGA	240
Ile Pro Lys Asp Arg Arg Pro Thr Gly Lys Ser Trp Gly Lys Pro Gly	
65 70 75 80	
TAC CCT TGG CCC CTG TAC GGG AAT GAG GGC CTC GGC TGG GCA GGG TGG	288
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp	
85 90 95	
CTC CTG TCC CCC CGA GGG TCT CGC CCG TCA TGG GGC CCA ACT GAC CCC	336
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro	
100 105 110	
CGG CAC AGG TCA CGC AAC TTG GGT AAG GTC ATC GAT ACC CTT ACG TGT	384
Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys	
115 120 125	
GGC TTT GCC GAC CTC ATG GGG TAC ATC CCT GTC GTC GGC GCC CCA GTT	432
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val	
130 135 140	
GGT GGT GTC GCC AGA GCT CTC GCG CAT GGC GTG AGA GTT CTG GAA GAC	480
Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp	
145 150 155 160	

GGG ATA AAC TAT GCA ACA GGG AAC TTG CCC GGT TGC TCC TTT TCT ATC Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile 165 170 175	528
TTC TTA TTG GCC CTG CTA TCT TGT ATC ACT GTG CCG GTC TCC GGC TTG Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Gly Leu 180 185 190	576
CAG GTC AAG AAC ACC AGC AGC TCT TAC ATG GTA ACC AAT GAC TGC CAG Gln Val Lys Asn Thr Ser Ser Ser Tyr Met Val Thr Asn Asp Cys Gln 195 200 205	624
AAC AGT AGC ATC GTC TGG CAG CTC AGG GAT GCT GTT CTT CAC GTC CCC Asn Ser Ser Ile Val Trp Gln Leu Arg Asp Ala Val Leu His Val Pro 210 215 220	672
GGG TGT GTC CCT TGT GAG GAG AAG GGC AAC ATA TCC CGC TGT TGG ATA Gly Cys Val Pro Cys Glu Glu Lys Gly Asn Ile Ser Arg Cys Trp Ile 225 230 235 240	720
CCG GTT TCG CCC AAT ATA GCT GTG AGC CAA CCT GGT GCG CTT ACC AAG Pro Val Ser Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Leu Thr Lys 245 250 255	768
GGC CTG CGG ACG CAT ATT GAT ACC ATC ATT GCA TCC GCT ACG TTT TGC Gly Leu Arg Thr His Ile Asp Thr Ile Ile Ala Ser Ala Thr Phe Cys 260 265 270	816
TCT GCC CTG TAC ATA GGA GAC CTG TGT GGC GCG GTG ATG TTG GCT TCT Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Ala Val Met Leu Ala Ser 275 280 285	864
CAA GTC TTC ATC ATC TCG CCC CAG CAT CAT AAG TTT GTC CAG GAC TGC Gln Val Phe Ile Ile Ser Pro Gln His His Lys Phe Val Gln Asp Cys 290 295 300	912
AAC TGT TCC ATA TAC CCA GGC CAC ATC ACT GGA CAT CGG ATG GCG Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala 305 310 315	957

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
 35 40 45
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60
 Ile Pro Lys Asp Arg Arg Pro Thr Gly Lys Ser Trp Gly Lys Pro Gly
 65 70 75 80
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val
 130 135 140
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160
 Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
 165 170 175
 Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Gly Leu
 180 185 190
 Gln Val Lys Asn Thr Ser Ser Ser Tyr Met Val Thr Asn Asp Cys Gln
 195 200 205
 Asn Ser Ser Ile Val Trp Gln Leu Arg Asp Ala Val Leu His Val Pro
 210 215 220
 Gly Cys Val Pro Cys Glu Glu Lys Gly Asn Ile Ser Arg Cys Trp Ile
 225 230 235 240
 Pro Val Ser Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Leu Thr Lys
 245 250 255
 Gly Leu Arg Thr His Ile Asp Thr Ile Ile Ala Ser Ala Thr Phe Cys
 260 265 270
 Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Ala Val Met Leu Ala Ser
 275 280 285
 Gln Val Phe Ile Ile Ser Pro Gln His His Lys Phe Val Gln Asp Cys
 290 295 300
 Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 1:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 2..337

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

C TCA ACG GTC ACG GAG AGG GAC ATC AGA ACT GAG GAG TCC ATA TAC	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr	
1 5 10 15	
CTT GCT TGC TCT TTA CCC GAG CAG GCA CGG ACT GCC ATA CAC TCA CTG	94
Leu Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu	
20 25 30	
ACT GAG AGG CTT TAC GTG GGA GGG CCC ATG CTA AAC AGC AAA GGG CAA	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Leu Asn Ser Lys Gly Gln	
35 40 45	
ACC TGC GGA TAC AGA CGC TGC CGC GCC AGC GGA GTG TTC ACC ACT AGC	190
Thr Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser	
50 55 60	
ATG GGA AAT ACC ATC ACG TGC TAC GTG AAG GCA CAA GCA GCC TGT AAG	238
Met Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Gln Ala Ala Cys Lys	
65 70 75	
GCT GCG GGC ATA ATT GCC CCC ACG ATG CTG GTG TGC GGC GAC GAT CTA	286
Ala Ala Gly Ile Ile Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTT GTC ATC TCA GAG AGT CAG GGG ACC GAG GAG GAC GAG CGG AAC CTA	334
Val Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu	
100 105 110	
CGA GCC	340
Arg Ala	

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

```

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu
 1             5             10             15
Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr
      20             25             30
Glu Arg Leu Tyr Val Gly Gly Pro Met Leu Asn Ser Lys Gly Gln Thr
      35             40             45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met
      50             55             60
Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Gln Ala Ala Cys Lys Ala
      65             70             75             80
Ala Gly Ile Ile Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
      85             90             95
Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu Arg
      100            105            110
Ala
  
```

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..345

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

ATG AGC ACA CTT CCT AAA CCA CAA AGA AAA ACC AAA AGA AAC ACC AAC

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15
 CCC GGC CAC AGG ACG TTA AGT TCC CAG GCG GCG GTC AGA TCG TTG GTG 96
 Pro Gly His Arg Thr Leu Ser Ser Gln Ala Ala Val Arg Ser Leu Val
 20 25 30
 GAG TTT ACG TGC TAC CAC GCA GGG GCC CCC AGT TGG GTG TGC GTG CAG 144
 Glu Phe Thr Cys Tyr His Ala Gly Ala Pro Ser Trp Val Cys Val Gln
 35 40 45
 TGC GCA AGA CTT CCG AGC GGT CGC AAC CTC GCA GTA GGC GCC AAC CCA 192
 Cys Ala Arg Leu Pro Ser Gly Arg Asn Leu Ala Val Gly Ala Asn Pro
 50 55 60
 TCC CCA GGG CGC GCC GAA CCG AGG GCA GGT CCT GGG CTC AGC CCG GGT 240
 Ser Pro Gly Arg Ala Glu Pro Arg Ala Gly Pro Gly Leu Ser Pro Gly
 65 70 75 80
 ACC CTT GGC CCC TAT ATG GGA ATG AGG GCT GCG GGT GGG CAG GGT GGC 288
 Thr Leu Gly Pro Tyr Met Gly Met Arg Ala Ala Gly Gly Gln Gly Gly
 85 90 95
 TCC TGT CCC CGC GCG GCT CTC GCC CGT CGT GGG GCC CAA ATG ACC CCC 336
 Ser Cys Pro Arg Ala Ala Leu Ala Arg Arg Gly Ala Gln Met Thr Pro
 100 105 110
 GGC GCA GGA 345
 Gly Ala Gly
 115

(2) INFORMATION FOR SEQ ID NO: 148:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15
 Pro Gly His Arg Thr Leu Ser Ser Gln Ala Ala Val Arg Ser Leu Val
 20 25 30
 Glu Phe Thr Cys Tyr His Ala Gly Ala Pro Ser Trp Val Cys Val Gln
 35 40 45
 Cys Ala Arg Leu Pro Ser Gly Arg Asn Leu Ala Val Gly Ala Asn Pro
 50 55 60
 Ser Pro Gly Arg Ala Glu Pro Arg Ala Gly Pro Gly Leu Ser Pro Gly
 65 70 75 80
 Thr Leu Gly Pro Tyr Met Gly Met Arg Ala Ala Gly Gly Gln Gly Gly

85

90

95

Ser Cys Pro Arg Ala Ala Leu Ala Arg Arg Gly Ala Gln Met Thr Pro
 100 105 110

Gly Ala Gly
 115

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..280

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

G GCC TGT GAC CTC AAG GAC GAG GCT AGG AGG GTG ATA ACT TCA CTC	46
Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu	
1 5 10 15	
ACG GAG CGG CTT TAC TGT GGT GGT CCT ATG TTC AAC AGC AAG GGA CAA	94
Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln	
20 25 30	
CAC TGC GGT TAC CGC CGC TGC CGT GCT AGT GGG GTG CTA CCC ACC AGC	142
His Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser	
35 40 45	
TTC GGG AAC ACA ATC ACC TGT TAC ATC AAA GCA AAG GCA GCT ACC AAA	190
Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys	
50 55 60	
GCT GCC GGA ATT AAA AAT CCA TCA TTC CTT GTC TGC GGA GAT GAC TTG	238
Ala Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu	
65 70 75	
GTC GTG ATT GCT GAG AGT GCA GGG ATC GAT GAG GAC AGA GCG	280
Val Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Arg Ala	
80 85 90	

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

```

Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu Thr
 1             5             10             15
Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln His
          20             25             30
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe
          35             40             45
Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys Ala
          50             55             60
Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu Val
          65             70             75             80
Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Arg Ala
          85             90

```

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 499 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..499

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

```

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC AAC      48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1             5             10             15
CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGC      96
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
          20             25             30

```

[illegible]

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5					10					15	
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly
			20					25					30		
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Met	Gly	Val	Arg	Ala
		35					40					45			

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60
 Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly
 65 70 75 80
 Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp
 85 90 95
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile
 130 135 140
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
 145 150 155 160
 Gly Val Asn Tyr Ala Thr
 165

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

ACG TGC GGA TTC GCC GAT CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly	
1 5 10 15	
CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu	
20 25 30	
GAG GAC GGG GTA AAC TAT CCA ACA GGG AAT TTA CCC GGT TGC TCT TTC	144

Glu Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC TCT	192
Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCA GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT GAT	240
Ala Val. Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His	
85 90 95	
GCA CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA TGC	336
Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys	
100 105 110	
TGG GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA GTC	384
Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val	
115 120 125	
ACG GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT GCC	432
Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala	
130 135 140	
CTC TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC TTG	480
Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu	
145 150 155 160	
GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG CAG	528
Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln	
165 170 175	
AAC TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG ATG	576
Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met	
180 185 190	
GCG	579
Ala	

(2) INFORMATION FOR SEQ ID NO: 154:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
 20 25 30
 Glu Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45
 Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
 50 55 60
 Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
 65 70 75 80
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His
 85 90 95
 Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys
 100 105 110
 Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val
 115 120 125
 Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala
 130 135 140
 Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
 145 150 155 160
 Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
 165 170 175
 Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met
 180 185 190
 Ala

(2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

ACG TGC GGA TTC GCC GAC CTC GTG GGG TAC ATC CCG CTC GTA GGC GGC	48
Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly	
1 5 10 15	
CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAT GGT GTG AGG GTT CTT	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu	
20 25 30	
GAG GAC GGG GTG AAT TAT GCA ACA GGG AAT CTG CCT GGT TGC TCT TTC	144
Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC ATT CTT GCA CTT CTC TCG TGC CTC ACT GTC CCG GCC TCT	192
Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCA GTT CCC TAC CGA AAT GCC TCT GGG ATC TAT CAT GTC ACC AAT GAT	240
Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT GAT CTG ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His	
85 90 95	
GCA CCT GGC TGC GTG CCT TGT GTC AGG AAA GAT AAT GTG AGT AGG TGC	336
Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys	
100 105 110	
TGG GTC CAA ATT ACC CCC ACG CTG TCA GCC CCG AGC TTC GGA GCA GTC	384
Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val	
115 120 125	
ACG GCT CCC CTT CGG AGA GCC GTT GAT TAC TTG GTG GGA GGG GCT GCC	432
Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala	
130 135 140	
CTC TGC TCC GCG TTA TAC GTT GGA GAC GCG TGT GGG GCA CTA TTT TTG	480
Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu	
145 150 155 160	
GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAT GCT ACG GTG CAG	528
Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln	
165 170 175	
GAC TGC AAC TGT TCC ATC TAC AGT GGC CAC GTC ACC GGC CAT CAG ATG	576
Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met	
180 185 190	
GCA	579
Ala	

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly
 1 5 10 15
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
 20 25 30
 Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45
 Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
 50 55 60
 Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp
 65 70 75 80
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His
 85 90 95
 Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys
 100 105 110
 Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val
 115 120 125
 Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala
 130 135 140
 Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu
 145 150 155 160
 Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
 165 170 175
 Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met
 180 185 190
 Ala

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..530

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 3..527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

CA CCT ACG ACA GCT CTG CTG GTG GCC CAG TTA CTG CGG ATT CCC CAA	47
Pro Thr Thr Ala Leu Leu Val Ala Gln Leu Leu Arg Ile Pro Gln	
1 5 10 15	
GTG GTC ATT GAC ATC ATC GCA GGG AGC CAC TGG GGG GTC TTG TTT GCC	95
Val Val Ile Asp Ile Ile Ala Gly Ser His Trp Gly Val Leu Phe Ala	
20 25 30	
GCC GCA TAC TAT GCA TCG GTG GCT AAC TGG ACC AAG GTC GTG CTG GTC	143
Ala Ala Tyr Tyr Ala Ser Val Ala Asn Trp Thr Lys Val Val Leu Val	
35 40 45	
TTG TTT CTG TTT GCA GGG GTT GAT GCT ACT ACC CAG ATT TCG GGC GGC	191
Leu Phe Leu Phe Ala Gly Val Asp Ala Thr Thr Gln Ile Ser Gly Gly	
50 55 60	
TCC AGC GCC CAA ACG ACG TAT GGC ATC GCC TCA TTT ATC ACC CGC GGC	239
Ser Ser Ala Gln Thr Thr Tyr Gly Ile Ala Ser Phe Ile Thr Arg Gly	
65 70 75	
GCG CAG CAG AAA CTG CAG CTC ATA AAT ACC AAC GGA AGC TGG CAC ATC	287
Ala Gln Gln Lys Leu Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile	
80 85 90 95	
AAC AGG ACC GCC CTT AAT TGT AAT GAC AGC CTC CAG ACT GGG TTC ATA	335
Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Ile	
100 105 110	
GCC GGC CTC TTC TAC TAC CAT AAG TTC AAC TCT TCT GGA TGC CCG GAT	383
Ala Gly Leu Phe Tyr Tyr His Lys Phe Asn Ser Ser Gly Cys Pro Asp	
115 120 125	
CGG ATG GCT AGC TGT AGG GCC CTT GCC ACT TTT GAC CAG GGC TGG GGA	431
Arg Met Ala Ser Cys Arg Ala Leu Ala Thr Phe Asp Gln Gly Trp Gly	
130 135 140	
ACT ATC AGC TAT GCC AAC ATA TCG GGT CCC AGT GAT GAC AAA CCA TAT	479
Thr Ile Ser Tyr Ala Asn Ile Ser Gly Pro Ser Asp Asp Lys Pro Tyr	
145 150 155	
TGC TGG CAC TAT CCC CCA CGG CCG TGC GGA GTG GTG CCA GCC CAA GAG	527

Cys Trp His Tyr Pro Pro Arg Pro Cys Gly Val Val Pro Ala Gln Glu
 160 165 170 175

GTC
 Val

530

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

Pro Thr Thr Ala Leu Leu Val Ala Gln Leu Leu Arg Ile Pro Gln Val
 1 5 10 15
 Val Ile Asp Ile Ile Ala Gly Ser His Trp Gly Val Leu Phe Ala Ala
 20 25 30
 Ala Tyr Tyr Ala Ser Val Ala Asn Trp Thr Lys Val Val Leu Val Leu
 35 40 45
 Phe Leu Phe Ala Gly Val Asp Ala Thr Thr Gln Ile Ser Gly Gly Ser
 50 55 60
 Ser Ala Gln Thr Thr Tyr Gly Ile Ala Ser Phe Ile Thr Arg Gly Ala
 65 70 75 80
 Gln Gln Lys Leu Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile Asn
 85 90 95
 Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Ile Ala
 100 105 110
 Gly Leu Phe Tyr Tyr His Lys Phe Asn Ser Ser Gly Cys Pro Asp Arg
 115 120 125
 Met Ala Ser Cys Arg Ala Leu Ala Thr Phe Asp Gln Gly Trp Gly Thr
 130 135 140
 Ile Ser Tyr Ala Asn Ile Ser Gly Pro Ser Asp Asp Lys Pro Tyr Cys
 145 150 155 160
 Trp His Tyr Pro Pro Arg Pro Cys Gly Val Val Pro Ala Gln Glu Val
 165 170 175

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

C TCG ACC GTT ACC GAA CAT GAC ATA ATG ACC GAA GAG TCC ATT TAC	46
Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu Ser Ile Tyr	
1 5 10 15	
CAA TCA TGT GAC TTG CAG CCC GAG GCA CGC GCA GCA ATA CGG TCA CTC	94
Gln Ser Cys Asp Leu Gln Pro Glu Ala Arg Ala Ala Ile Arg Ser Leu	
20 25 30	
ACC CAA CGC CTC TAC TGT GGA GGC CCC ATG TAC AAC AGC AAG GGG CAA	142
Thr Gln Arg Leu Tyr Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln	
35 40 45	
CAG TGT GGT TAT CGC AGA TGC CGC GCC AGC GGC GTT TTC ACC ACC AGT	190
Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser	
50 55 60	
ATG GGC AAC ACC ATG ACG TGC TAC ATC AAG GCT TTA GCC TCC TGT AGA	238
Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg	
65 70 75	
GCC GCA AGG CTC CGG GAC TGC ACG CTC CTG GTG TGT GGT GAC GAT CTT	286
Ala Ala Arg Leu Arg Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTG GCC ATC TGC GAG AGC CAG GGG ACA CAC GAG GAT GAA GCA AGC CTG	334
Val Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Ser Leu	
100 105 110	
AGA GCC	340
Arg Ala	

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu Ser Ile Tyr Gln
 1 5 10 15

Ser Cys Asp Leu Gln Pro Glu Ala Arg Ala Ala Ile Arg Ser Leu Thr
 20 25 30

Gln Arg Leu Tyr Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln
 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met
 50 55 60

Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg Ala
 65 70 75 80

Ala Arg Leu Arg Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu Val
 85 90 95

Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Ser Leu Arg
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

C TCA ACC GCC ACC GAA CAT GAC ATA TTG ACT GAA GAG TCC ATA TAC
 Ser Thr Ala Thr Glu His Asp Ile Leu Thr Glu Glu Ser Ile Tyr

46

1	5	10	15	
CAA TCA TGT GAC TCG CAG CCC GAC GCA CGC GCA GCA ATA CGG TCA CTC				94
Gln Ser Cys Asp Ser Gln Pro Asp Ala Arg Ala Ala Ile Arg Ser Leu				
	20	25	30	
ACC CAA CGC TTG TTC TGT GGA GGC CCC ATG TAT AAC AGC AAG GGG CAA				142
Thr Gln Arg Leu Phe Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln				
	35	40	45	
CAA TGT GGT TAT CGC AGA TGC CGC GCC AGC GGC GTC TTC ACC ACC AGT				190
Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser				
	50	55	60	
ATG GGC AAC ACC ATG ACG TGC TAC ATT AAG GCT TTA GCC TCC TGT AGA				238
Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg				
	65	70	75	
ACC GCT GGG CTC CGG GAC TAC ACG CTC CTG GTG TGT GGT GAC GAT CAT				286
Thr Ala Gly Leu Arg Asp Tyr Thr Leu Leu Val Cys Gly Asp Asp His				
	80	85	90	95
GTG GCC ATC TGC GAG AGC CAG GGG ACA CAC GAG GAT GAA GCG AAC CTG				334
Val Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Asn Leu				
	100	105	110	
AGA GCC				340
Arg Ala				

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Ser Thr Ala Thr Glu His Asp Ile Leu Thr Glu Glu Ser Ile Tyr Gln				
1	5	10	15	
Ser Cys Asp Ser Gln Pro Asp Ala Arg Ala Ala Ile Arg Ser Leu Thr				
	20	25	30	
Gln Arg Leu Phe Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln				
	35	40	45	
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met				
	50	55	60	
Gly Asn Thr Met Thr Cys Tyr Ile-Lys Ala Leu Ala Ser Cys Arg Thr				
	65	70	75	80
Ala Gly Leu Arg Asp Tyr Thr Leu Leu Val Cys Gly Asp Asp His Val				
	85	90	95	

Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Asn Leu Arg
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..499

(ix) FEATURE:

- ```
(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..496
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | AGC | ACG | AAT | CCT | AAA | CTT | CAA | AGA | AAA | ACC | AAA | CGT | AAC | ACC | AAC | 48  |
| Met | Ser | Thr | Asn | Pro | Lys | Leu | Gln | Arg | Lys | Thr | Lys | Arg | Asn | Thr | Asn |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| CGC | CGC | CCC | ATG | GAC | GTT | AAG | TTC | CCG | GGT | GGT | GGC | CAG | ATC | GTT | GGC | 96  |
| Arg | Arg | Pro | Met | Asp | Val | Lys | Phe | Pro | Gly | Gly | Gly | Gln | Ile | Val | Gly |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| GGA | GTT | TAC | TTG | TTG | CCG | CGC | AGG | GGC | CCT | AGG | TTG | GGT | GTG | CGC | GCG | 144 |
| Gly | Val | Tyr | Leu | Leu | Pro | Arg | Arg | Gly | Pro | Arg | Leu | Gly | Val | Arg | Ala |     |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| ACT | CGG | AAG | ACT | TCG | GAG | CGG | TCG | CAA | CCT | CGT | GGG | AGG | CGC | CAA | CCT | 192 |
| Thr | Arg | Lys | Thr | Ser | Glu | Arg | Ser | Gln | Pro | Arg | Gly | Arg | Arg | Gln | Pro |     |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| ATC | CCC | AAG | GCG | CGC | CGA | TCC | GAG | GGC | AGA | TCC | TGG | GCG | CAG | CCC | GGG | 240 |
| Ile | Pro | Lys | Ala | Arg | Arg | Ser | Glu | Gly | Arg | Ser | Trp | Ala | Gln | Pro | Gly |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| TAT | CCT | TGG | CCC | CTT | TAC | GGC | AAT | GAG | GGC | TGT | GGG | TGG | GCA | GGG | TGG | 288 |
| Tyr | Pro | Trp | Pro | Leu | Tyr | Gly | Asn | Glu | Gly | Cys | Gly | Trp | Ala | Gly | Trp |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| CTC | CTG | TCC | CCT | CGC | GGG | TCT | CGG | CCG | TCT | TGG | GGC | CCT | AAT | GAT | CCC | 336 |

[illegible]



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| Leu | Leu | Ser | Pro | Arg | Gly | Ser | Arg | Pro | Ser | Trp | Gly | Pro | Asn | Asp | Pro |  |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |     |
| CGG | CGG | AGG | TCC | CGC | AAC | CTG | GGT | AAG | GTC | ATC | GAT | ACC | CTA | ACA | TGC |  | 384 |
| Arg | Arg | Arg | Ser | Arg | Asn | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys |  |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |     |
| GGC | TTC | GCC | GAC | CTC | ATG | GGA | TAC | ATC | CCG | CTT | GTA | GGC | GCC | CCC | GTG |  | 432 |
| Gly | Phe | Ala | Asp | Leu | Met | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Val |  |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |     |
| GGT | GGC | GTC | GCC | AGA | GCC | CTG | GCA | CAC | GGT | GTT | AGG | GCT | GTG | GAA | GAC |  | 480 |
| Gly | Gly | Val | Ala | Arg | Ala | Leu | Ala | His | Gly | Val | Arg | Ala | Val | Glu | Asp |  |     |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |  |     |
| GGG | ATC | AAC | TAC | GCA | ACA | G   |     |     |     |     |     |     |     |     |     |  | 499 |
| Gly | Ile | Asn | Tyr | Ala | Thr |     |     |     |     |     |     |     |     |     |     |  |     |
|     |     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |  |     |

## (2) INFORMATION FOR SEQ ID NO: 164:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Ser | Thr | Asn | Pro | Lys | Leu | Gln | Arg | Lys | Thr | Lys | Arg | Asn | Thr | Asn |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Arg | Arg | Pro | Met | Asp | Val | Lys | Phe | Pro | Gly | Gly | Gly | Gln | Ile | Val | Gly |  |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Gly | Val | Tyr | Leu | Leu | Pro | Arg | Arg | Gly | Pro | Arg | Leu | Gly | Val | Arg | Ala |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Thr | Arg | Lys | Thr | Ser | Glu | Arg | Ser | Gln | Pro | Arg | Gly | Arg | Arg | Gln | Pro |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Ile | Pro | Lys | Ala | Arg | Arg | Ser | Glu | Gly | Arg | Ser | Trp | Ala | Gln | Pro | Gly |  |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |  |
| Tyr | Pro | Trp | Pro | Leu | Tyr | Gly | Asn | Glu | Gly | Cys | Gly | Trp | Ala | Gly | Trp |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |  |
| Leu | Leu | Ser | Pro | Arg | Gly | Ser | Arg | Pro | Ser | Trp | Gly | Pro | Asn | Asp | Pro |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Arg | Arg | Arg | Ser | Arg | Asn | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Gly | Phe | Ala | Asp | Leu | Met | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Val |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp  
145 150 155 160

Gly Ile Asn Tyr Ala Thr  
165

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGTA ACACCAACCG CCGCCCTATG 60  
GACGTTAAGT TCCCAGGCGG TGGTCAGATC GTTGGCGGAG TTTACTTGTT GCCGCGCAGG 120  
GGCCCCAGGT TGGGTGTGCG CGCGACTCGG AAGACTTCGG AGCGGTCGCA ACCTCGTGGG 180  
AGGCGCCAAC CTATCCCCAA GGCGCGCCGA ACCGAGGGCA GATCCTGGGC GCAGCCCGGG 240  
TATCCTTGGC CCCTTTACGG CAATGAGGGC TGTGGGTGGG CAGGGTGGCT CCTGTCCCCT 300  
CGCGGNTCTC GGNCGTCTTG GGGCCCCAAT GATCCCCGNN GGAGATCCCC CAACTTGGGT 360  
AAGGTCATCG ATACCTAAC ATGCGGCTTC GCCGACCTCA TGGGATACAT CCCGCTTGTA 420  
GGCGCCCCCG TGGGTGGCGT CGCCAGGGCC CTGGCACATG GTGTTAGGGC TGTGGAAGAC 480  
GGGATCAATT ATGCAACAG 499

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn

|                                                                 |     |     |    |
|-----------------------------------------------------------------|-----|-----|----|
| 1                                                               | 5   | 10  | 15 |
| Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly |     |     |    |
| 20                                                              | 25  | 30  |    |
| Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala |     |     |    |
| 35                                                              | 40  | 45  |    |
| Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro |     |     |    |
| 50                                                              | 55  | 60  |    |
| Ile Pro Lys Ala Arg Arg Thr Glu Gly Arg Ser Trp Ala Gln Pro Gly |     |     |    |
| 65                                                              | 70  | 75  | 80 |
| Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp |     |     |    |
| 85                                                              | 90  | 95  |    |
| Leu Leu Ser Pro Arg Xaa Ser Arg Xaa Ser Trp Gly Pro Asn Asp Pro |     |     |    |
| 100                                                             | 105 | 110 |    |
| Arg Xaa Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu         |     |     |    |
| 115                                                             | 120 | 125 |    |

## (2) INFORMATION FOR SEQ ID NO: 167:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..579

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ACA TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTA GGC GCC | 48  |
| Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala |     |
| 1 5 10 15                                                       |     |
| CCC GTG GGT GGC GTC GCC AGG GCC-CTG GCA CAT GGT GTT AGG GCT GTG | 96  |
| Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val |     |
| 20 25 30                                                        |     |
| GAA GAC GGG ATC AAT TAT GCA ACA GGG AAC CTT CCC GGT TGC TCC TTT | 144 |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe |     |
| 35 40 45                                                        |     |
| TCT ATC TTC CTC TTG GCG CTC CTC TCG TGC CTG ACT GTT CCC ACA TCG | 192 |
| Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser |     |
| 50 55 60                                                        |     |
| GCC GTT AAC TAT CGC AAT GCT TCG GGC ATT TAT CAC ATC ACC AAT GAC | 240 |
| Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp |     |
| 65 70 75 80                                                     |     |
| TGC CCG AAT GCA AGC ATA GTG TAC GAG ACC GAA AAT CAC ATC TTA CAC | 288 |
| Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His |     |
| 85 90 95                                                        |     |
| CTC CCA GGG TGC GTA CCC TGT GTG AGG ACT GGG AAC CAG TCG CGG TGT | 336 |
| Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys |     |
| 100 105 110                                                     |     |
| TGG GTG GCC CTC ACT CCC ACA GTA GCG TCG CCA TAC GCC GGT GCT CCG | 384 |
| Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro |     |
| 115 120 125                                                     |     |
| CTT GAG CCC TTG CGG CGT CAT GTG GAC CTG ATG GTA GGT GCT GCC ACC | 432 |
| Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr |     |
| 130 135 140                                                     |     |
| ATG TGT TCC GCC CTC TAC ATC GGC GAC TTG TGC GGT GGC TTA TTC TTG | 480 |
| Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu |     |
| 145 150 155 160                                                 |     |
| GTG GGC CAA ATG TTC ACC TTC CAA CCG CGA CGT CAC TGG ACC ACT CAG | 528 |
| Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln |     |
| 165 170 175                                                     |     |
| GAC TGC AAT TGT TCC ATC TAC ACG GGC CAC ATT ACG GGT CAT CGG ATG | 576 |
| Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met |     |
| 180 185 190                                                     |     |
| GCA                                                             | 579 |
| Ala                                                             |     |

## (2) INFORMATION FOR SEQ ID NO: 168:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

|                                                                 |
|-----------------------------------------------------------------|
| Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala |
| 1 5 10 15                                                       |

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
                   20                                  25                                  30  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
                   35                                  40                                  45  
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser  
                   50                                  55                                  60  
 Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
                   65                                  70                                  75                                  80  
 Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His  
                                   85                                  90                                  95  
 Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys  
                                   100                                  105                                  110  
 Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro  
                   115                                  120                                  125  
 Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
                   130                                  135                                  140  
 Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu  
                   145                                  150                                  155                                  160  
 Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
                                   165                                  170                                  175  
 Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met  
                                   180                                  185                                  190  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..579
- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide
  - (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ACA TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTA GGC GCC | 48  |
| Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala |     |
| 1 5 10 15                                                       |     |
| CCC GTG GGT GGC GTC GCC AGA GCC CTG GCA CAC GGT GTT AGG GCT GTG | 96  |
| Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val |     |
| 20 25 30                                                        |     |
| GAA GAC GGG ATC AAC TAC GCA ACA GGG AAT CTC CCC GGT TGC TCC TTT | 144 |
| Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe |     |
| 35 40 45                                                        |     |
| TCT ATC TTC CTC TTG GCA CTT CTC TCG TGC CTC ACT GTT CCC GCG TCG | 192 |
| Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser |     |
| 50 55 60                                                        |     |
| GGC GTT AAC TAT CGC AAT GCT TCG GGC GTT TAT CAC ATC ACC AAC GAC | 240 |
| Gly Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp |     |
| 65 70 75 80                                                     |     |
| TGC CCG AAT GCG AGC ATA GTG TAC GAG ACC GAC AAT CAC ATC TTA CAC | 288 |
| Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Asp Asn His Ile Leu His |     |
| 85 90 95                                                        |     |
| CTC CCA GGG TGC GTA CCC TGT GTG AAG ACC GGG AAC CAG TCG CGG TGT | 336 |
| Leu Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys |     |
| 100 105 110                                                     |     |
| TGG GTG GCC CTC ACT CCC ACA GTG GCG TCG CCT TAC GTC GGT GCT CCG | 384 |
| Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Val Gly Ala Pro |     |
| 115 120 125                                                     |     |
| CTC GAG CCC TTG CGG CGC CAT GTG GAC CTG ATG GTA GGT GCT GCC ACC | 432 |
| Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr |     |
| 130 135 140                                                     |     |
| GTG TGC TCC GCC CTC TAC GTC GGC GAC CTG TGC GGT GGC TTA TTC TTG | 480 |
| Val Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu |     |
| 145 150 155 160                                                 |     |
| GTA GGC CAA ATG TTC ACC TTC CAA CCG CGA CGC CAC TGG ACG ACC CAG | 528 |
| Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln |     |
| 165 170 175                                                     |     |
| GAC TGT AAT TGT TCC ATC TAC GCA GGG CAT ATT ACG GGC CAT CGG ATG | 576 |
| Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met |     |
| 180 185 190                                                     |     |
| GCT                                                             | 579 |
| Ala                                                             |     |

(2) INFORMATION FOR SEQ ID NO: 170:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 Gly Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Asp Asn His Ile Leu His  
 85 90 95  
 Leu Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys  
 100 105 110  
 Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Val Gly Ala Pro  
 115 120 125  
 Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140  
 Val Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met  
 180 185 190  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 171:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..579

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ACA TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTG GGC GCC | 48  |
| Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala |     |
| 1 5 10 15                                                       |     |
| CCT GTT GGT GGC GTC GCC AGA GCC CTT GCG CAC GGC GTC AGG GCT GTG | 96  |
| Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val |     |
| 20 25 30                                                        |     |
| GAA GAC GGG ATT AAC TAT GCA ACA GGG AAC CTT CCT GGT TGC TCC TTT | 144 |
| Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe |     |
| 35 40 45                                                        |     |
| TCT ATC TTC CTT CTG GCA CTT CTC TCG TGC CTG ACT GTC CCC GCC TCG | 192 |
| Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser |     |
| 50 55 60                                                        |     |
| GCT GTG CAT TAT CAC AAC ACC TCG GGC ATC TAC CAC CTC ACC AAT GAC | 240 |
| Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Leu Thr Asn Asp |     |
| 65 70 75 80                                                     |     |
| TGC CCT AAC TCT AGC ATA GTC TTT GAG GCA GTC CAT CAC ATC TTG CAC | 288 |
| Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Val His His Ile Leu His |     |
| 85 90 95                                                        |     |
| CTT CCA GGA TGC GTC CCT TGT GTA AGA ACT GGG AAC CAG TCT CGG TGC | 336 |
| Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys |     |
| 100 105 110                                                     |     |
| TGG GTA GCC TTG ACC CCC ACG CTG GCC GCG CCA TAC CTT GGC GCT CCA | 384 |
| Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro Tyr Leu Gly Ala Pro |     |
| 115 120 125                                                     |     |
| CTC GAG TCC ATG CGG CGT CAC GTG GAT TTG ATG GTG GGC ACT GCT ACA | 432 |
| Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr |     |
| 130 135 140                                                     |     |
| TTG TGC TCA GCA CTC TAC GTT GGG GAC CTG TGC GGG GGC ATA TTC CTA | 480 |
| Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ile Phe Leu |     |
| 145 150 155 160                                                 |     |
| GCG GGC CAG ATG TTC ACC TTC CGG CCC CGC CTC CAT TGG ACC ACC CAG | 528 |
| Ala Gly Gln Met Phe Thr Phe Arg Pro Arg Leu His Trp Thr Thr Gln |     |
| 165 170 175                                                     |     |



GAG TGC AAT TGT TCC ACC TAT CCG GGC CAC ATC ACG GGT CAT AGA ATG 576  
 Glu Cys Asn Cys Ser Thr Tyr Pro Gly His Ile Thr Gly His Arg Met  
           180                                  185                                  190

GCG 579  
 Ala

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
   1                                  5                                  10                                  15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
                                   20                                  25                                  30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
                                   35                                  40                                  45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
   50                                  55                                  60

Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Leu Thr Asn Asp  
   65                                  70                                  75                                  80

Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Val His His Ile Leu His  
                                   85                                  90                                  95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys  
                                   100                                  105                                  110

Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro Tyr Leu Gly Ala Pro  
                                   115                                  120                                  125

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr  
   130                                  135                                  140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ile Phe Leu  
   145                                  150                                  155                                  160

Ala Gly Gln Met Phe Thr Phe Arg Pro Arg Leu His Trp Thr Thr Gln  
                                   165                                  170                                  175

Glu Cys Asn Cys Ser Thr Tyr Pro Gly His Ile Thr Gly His Arg Met  
                                   180                                  185                                  190

Ala

## (2) INFORMATION FOR SEQ ID NO: 173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ACG | TGC | GGT | TCC | GCC | GAC | CTC | ATG | GGA | TAC | ATC | CCG | CTC | GTA | GGC | GCC | 48  |
| Thr | Cys | Gly | Ser | Ala | Asp | Leu | Met | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| CCT | GTG | GGT | GGC | GTC | GCC | AGG | GCC | TTG | GCG | CAT | GGC | GTC | AGG | GCT | GTG | 96  |
| Pro | Val | Gly | Gly | Val | Ala | Arg | Ala | Leu | Ala | His | Gly | Val | Arg | Ala | Val |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| GAG | GAC | GGG | ATA | AAC | TAT | GCA | ACA | GGG | AAC | CTT | CCT | GGT | TGC | TCT | TTT | 144 |
| Glu | Asp | Gly | Ile | Asn | Tyr | Ala | Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
| TCT | ATC | TTC | CTT | CTG | GCA | CTT | CTC | TCG | TGC | CTG | ACT | GTC | CCC | GCC | TCA | 192 |
| Ser | Ile | Phe | Leu | Leu | Ala | Leu | Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser |     |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| GCT | GTG | CAT | TAT | CAC | AAC | ACC | TCG | GGC | ATC | TAT | CAC | ATC | ACT | AAT | GAC | 240 |
| Ala | Val | His | Tyr | His | Asn | Thr | Ser | Gly | Ile | Tyr | His | Ile | Thr | Asn | Asp |     |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| TGC | CCT | AAC | TCT | AGC | ATA | GTC | TTT | GAG | GCA | GAG | CAT | CAC | ATC | TTG | CAT | 288 |
| Cys | Pro | Asn | Ser | Ser | Ile | Val | Phe | Glu | Ala | Glu | His | His | Ile | Leu | His |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| CTT | CCA | GGA | TGC | GTC | CCC | TGT | GTG | AGA | ACT | GGG | AAC | CAG | TCA | CGA | TGC | 336 |
| Leu | Pro | Gly | Cys | Val | Pro | Cys | Val | Arg | Thr | Gly | Asn | Gln | Ser | Arg | Cys |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| TGG | ATA | GCC | TTG | ACC | CCT | ACG | TTG | GCC | GCG | CCA | CAC | ATT | GGC | GCT | CCA | 384 |
| Trp | Ile | Ala | Leu | Thr | Pro | Thr | Leu | Ala | Ala | Pro | His | Ile | Gly | Ala | Pro |     |

| 115                                                             | 120 | 125 |     |
|-----------------------------------------------------------------|-----|-----|-----|
| CTT GAG TCC ATG CGA CGT CAT GTG GAT TTG ATG GTA GGC ACT GCC ACA |     |     | 432 |
| Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr |     |     |     |
| 130                                                             | 135 | 140 |     |
| TTG TGC TCC GCA CTC TAC ATT GGA GAT CTG TGC GGA GGC ATA TTT CTA |     |     | 480 |
| Leu Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ile Phe Leu |     |     |     |
| 145                                                             | 150 | 155 | 160 |
| GTG GGC CAG ATG TTC AAC TTC AGG CCC CGC CTG CAC TGG ACC ACC CAG |     |     | 528 |
| Val Gly Gln Met Phe Asn Phe Arg Pro Arg Leu His Trp Thr Thr Gln |     |     |     |
| 165                                                             | 170 | 175 |     |
| GAG TGC AAT TGT TCC ATC TAT CCA GGC CAC ATC ACG GGT CAC AGA ATG |     |     | 576 |
| Glu Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met |     |     |     |
| 180                                                             | 185 | 190 |     |
| GCG                                                             |     |     | 579 |
| Ala                                                             |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Thr Cys Gly Ser Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala |     |     |
| 1                                                               | 5   | 10  |
| Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val |     |     |
| 20                                                              | 25  | 30  |
| Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe |     |     |
| 35                                                              | 40  | 45  |
| Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser |     |     |
| 50                                                              | 55  | 60  |
| Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Ile Thr Asn Asp |     |     |
| 65                                                              | 70  | 75  |
| Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Glu His His Ile Leu His |     |     |
| 85                                                              | 90  | 95  |
| Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys |     |     |
| 100                                                             | 105 | 110 |
| Trp Ile Ala Leu Thr Pro Thr Leu Ala Ala Pro His Ile Gly Ala Pro |     |     |
| 115                                                             | 120 | 125 |

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr  
 130 135 140  
 Leu Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ile Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Asn Phe Arg Pro Arg Leu His Trp Thr Thr Gln  
 165 170 175  
 Glu Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met  
 180 185 190  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 175:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ACG TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC | 48  |
| Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala |     |
| 1 5 10 15                                                       |     |
| CCT GTG GGT GGC GTC GCC AGG GCC TTG GCA CAT GGT GTC AGG GCC GTG | 96  |
| Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val |     |
| 20 25 30                                                        |     |
| GAG GAC GGG ATT AAC TAT GCA ACA GGG AAT CTT CCC GGT TGC TCC TTT | 144 |
| Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe |     |
| 35 40 45                                                        |     |
| TCT ATC TTC CTT CTA GCA CTT CTC TCG TGC TTG ACT GTC CCG GCC TCG | 192 |
| Ser Ile Phe Leu Leu Ala Leu Ser Cys Leu Thr Val Pro Ala Ser     |     |
| 50 55 60                                                        |     |
| GCG CAG CAC TAC CGG AAC ATC TCG GGC ATT TAT CAC GTC ACC AAT GAC | 240 |
| Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp |     |

| 65                                                              | 70  | 75  | 80  |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| TGC CCG AAC TCT AGT ATA GTG TAT GAA GCT GAC CAT CAT ATC ATG CAT |     |     |     | 288 |
| Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His | 85  | 90  | 95  |     |
| CTA CCA GGG TGT GTG CCT TGC GTG AGA ACC GGG AAC ACC TCG CGC TGC |     |     |     | 336 |
| Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys | 100 | 105 | 110 |     |
| TGG GTT CCT TTA ACA CCC ACT GTG GCT GCC CCC TAT GTT GGC GCG CCG |     |     |     | 384 |
| Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro | 115 | 120 | 125 |     |
| CTC GAA TCC ATG CGG CGG CAC GTG GAC TTA ATG GTG GGT GCC GCC ACC |     |     |     | 432 |
| Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr | 130 | 135 | 140 |     |
| GTC TGC TCG GCC CTG TAC ATC GGA GAC CTT TGC GGA GGT GTC TTC CTG |     |     |     | 480 |
| Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu | 145 | 150 | 155 | 160 |
| GTC GGG CAG ATG TTC ACC TTC CGG CCG CGC CGC CAT TGG ACT ACC CAG |     |     |     | 528 |
| Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln | 165 | 170 | 175 |     |
| GAC TGC AAC TGC TCT ATC TAT GAT GGC CAC ATC ACC GGC CAT AGA ATG |     |     |     | 576 |
| Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg Met | 180 | 185 | 190 |     |
| GCT                                                             |     |     |     | 579 |
| Ala                                                             |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 176:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

```

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
 50 55 60

```

Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp  
 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His  
 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys  
 100 105 110

Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro  
 115 120 125

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
 145 150 155 160

Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg Met  
 180 185 190

Ala

## (2) INFORMATION FOR SEQ ID NO: 177:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

ACG TGC GGG TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCT 48  
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15

CCA GTA GGA GGC GTC GCC AGA GCC TTG GCG CAT GGC GTC AGG GCT GTG 96  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val

| 20                                                                                                                                                    | 25 | 30 |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|----|----|-----|
| GAG GAC GGG ATC AAT TAC GCA ACA GGG AAC CTT CCC GGC TGC TCC TTT<br>Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe<br>35 40 45        |    |    | 144 |
| TCT ATC TTC CTC TTG GTA CTT CTC TCG CGC CTA ACT GTC CCA GCG TCT<br>Ser Ile Phe Leu Leu Val Leu Leu Ser Arg Leu Thr Val Pro Ala Ser<br>50 55 60        |    |    | 192 |
| GCT CAG CAC TAC CGG AAT GCA TCG GGC ATC TAC CAT GTC ACC AAC GAC<br>Ala Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp<br>65 70 75 80     |    |    | 240 |
| TGC CCG AAC TCC AGT ATT GTG TAT GAA GCC GAC CAT CAC ATC ATG CAC<br>Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His<br>85 90 95        |    |    | 288 |
| CTA CCC GGG TGT GTG CCC TGT GTA AGA ACT GGG AAT GTC TCG CGT TGC<br>Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys<br>100 105 110     |    |    | 336 |
| TGG ATT CCT TTA ACA CCC ACT GTA GCC GTC CCC TAC CTC GGG GCT CCA<br>Trp Ile Pro Leu Thr Pro Thr Val Ala Val Pro Tyr Leu Gly Ala Pro<br>115 120 125     |    |    | 384 |
| CTT ACG TCT GTA CGG CAG CAT GTG GAC CTG ATG GTG GGG GCG GCC ACC<br>Leu Thr Ser Val Arg Gln His Val Asp Leu Met Val Gly Ala Ala Thr<br>130 135 140     |    |    | 432 |
| TTA TGC TCT GCC CTC TAC ATC GGA GAC CAT TGC GGA GGT GTC TTC TTG<br>Leu Cys Ser Ala Leu Tyr Ile Gly Asp His Cys Gly Gly Val Phe Leu<br>145 150 155 160 |    |    | 480 |
| GCA GGG CAG ATG GTC AGT TTC CAA CCC CGG CGT CAT TGG ACT ACC CAG<br>Ala Gly Gln Met Val Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln<br>165 170 175     |    |    | 528 |
| GAT TGC AAC TGT TCC ATC TAT GTG GGC CAC ATC ACC GGC CAC AGG ATG<br>Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met<br>180 185 190     |    |    | 576 |
| GCC<br>Ala                                                                                                                                            |    |    | 579 |

## (2) INFORMATION FOR SEQ ID NO: 178:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Leu Leu Val Leu Leu Ser Arg Leu Thr Val Pro Ala Ser  
 50 55 60  
 Ala Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His  
 85 90 95  
 Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys  
 100 105 110  
 Trp Ile Pro Leu Thr Pro Thr Val Ala Val Pro Tyr Leu Gly Ala Pro  
 115 120 125  
 Leu Thr Ser Val Arg Gln His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140  
 Leu Cys Ser Ala Leu Tyr Ile Gly Asp His Cys Gly Gly Val Phe Leu  
 145 150 155 160  
 Ala Gly Gln Met Val Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met  
 180 185 190  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

```

ACCTGCGGCT TCGCCGACCT CATGGGATAC ATCCCGCTCG TAGGCGCCCC CGTGGGAGGC 60
GTCGCCAGAR CTCTGGCGCA TGGCGTCAGG GCTCTGGAAG ACGGGATCAA TTATGCAACA 120
GGGAATCTTC CTGGTTGCTC TTTCTCTATC TCCCTTCTTG AACTTCTCTC GTGCCTGACT 180
GTTCCCGCCT CAGCCATCCA CTATCGCAAT GCTTCGGACG GTTATTATAT CACCAATGAT 240
TGCCCGAACT CTAGCATAGT GTATGAAGCC GAGAACCACA TCTTGACCT TCCGGGGTGT 300
ATACCCTGTG TGAAGACCGG GAATCAGTCG CGGTGCTGGG TGGCTCTCAC CCCCACGCTG 360
GCGGCCCCAC ACCTACGTGC TCCGCTTTCG TCCTTACGGG CGCATGTGGA CCTAATGGTG 420
GGGGCCGCCA CGGCATGCTC CGCTTTTAC ATTGGAGATC TGTGCGGGGG TGTGTTTTTG 480
GCGGGCCAAC TGTTCACTAT CCGGCCACGC ATTCATGAAA CCACTCAGGA CTGCAATTGC 540
TCCATCTACT CAGGGCACAT CACGGGTNNN NNNNNNNN 579

```

## (2) INFORMATION FOR SEQ ID NO: 180:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

```

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15
Pro Val Gly Gly Val Ala Arg Xaa Leu Ala His Gly Val Arg Ala Leu
20 25 30
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45
Ser Ile Ser Leu Leu Glu Leu Leu Ser Cys Leu Thr Val Pro Ala Ser
50 55 60
Ala Ile His Tyr Arg Asn Ala Ser Asp Gly Tyr Tyr Ile Thr Asn Asp
65 70 75 80
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Glu Asn His Ile Leu His
85 90 95
Leu Pro Gly Cys Ile Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys
100 105 110

```



GTGGGACAGA TGTTACCTT CCAGCCGCGC CGCCACTGGA CCACTCAGGA CTGCAACTGC 540  
 TCCATTTACG TCGGCCACAT CACAGGCCAC AGAATGGCT 579

## (2) INFORMATION FOR SEQ ID NO: 182:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Cys | Gly | Phe | Ala | Asp | Leu | Met | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | 1   | 5   | 10  | 15  |
| Pro | Val | Gly | Gly | Val | Ala | Arg | Ala | Leu | Ala | His | Gly | Val | Arg | Ala | Val | 20  | 25  | 30  |     |
| Glu | Asp | Gly | Ile | Asn | Tyr | Ala | Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | 35  | 40  | 45  |     |
| Ser | Ile | Xaa | Leu | Leu | Ala | Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | 50  | 55  | 60  |     |     |
| Ala | Gln | His | Tyr | Arg | Asn | Val | Ser | Gly | Ile | Tyr | His | Val | Thr | Asn | Asp | 65  | 70  | 75  | 80  |
| Cys | Pro | Asn | Ser | Ser | Ile | Val | Tyr | Glu | Ala | Asp | His | His | Ile | Met | His | 85  | 90  | 95  |     |
| Leu | Pro | Gly | Cys | Ile | Pro | Cys | Val | Arg | Thr | Gly | Asn | Val | Ser | Arg | Cys | 100 | 105 | 110 |     |
| Trp | Val | Ser | Leu | Thr | Pro | Thr | Val | Ala | Ala | Pro | Tyr | Leu | Gly | Ala | Pro | 115 | 120 | 125 |     |
| Leu | Thr | Ser | Leu | Arg | Arg | His | Val | Asp | Leu | Met | Val | Gly | Ala | Ala | Thr | 130 | 135 | 140 |     |
| Leu | Cys | Ser | Ala | Leu | Tyr | Val | Gly | Asp | Leu | Cys | Gly | Gly | Val | Phe | Leu | 145 | 150 | 155 | 160 |
| Val | Gly | Gln | Met | Phe | Thr | Phe | Gln | Pro | Arg | Arg | His | Trp | Thr | Thr | Gln | 165 | 170 | 175 |     |
| Asp | Cys | Asn | Cys | Ser | Ile | Tyr | Val | Gly | His | Ile | Thr | Gly | His | Arg | Met | 180 | 185 | 190 |     |
| Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..579

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ACC TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC | 48  |
| Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala |     |
| 1 5 10 15                                                       |     |
| CCT GTG GGT GGC GTC GCC AGG GCC CTA GAA CAC GGT GTT AGG GCT GTG | 96  |
| Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val |     |
| 20 25 30                                                        |     |
| GAG GAC GGT ATT AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTT | 144 |
| Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe |     |
| 35 40 45                                                        |     |
| TCT ATC TCC CTC TTG GCA CTT CTT TCG TGC CTG ACT GTT CCC ACC TCA | 192 |
| Ser Ile Ser Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser |     |
| 50 55 60                                                        |     |
| GCC GTC AAC TAT CGC AAC GCC TCG GGC GTC TAT CAT ATC ACC AAT GAC | 240 |
| Ala Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp |     |
| 65 70 75 80                                                     |     |
| TGC CCG AAT TCG AGC ATA GTG TAC GAG GCT GAC TAC CAC ATC CTA CAC | 288 |
| Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Tyr His Ile Leu His |     |
| 85 90 95                                                        |     |
| CTC CCT GGG TGC TTA CCC TGC GTG AGG GTT GGG AAT CAG TCA CGC TGC | 336 |
| Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys |     |
| 100 105 110                                                     |     |
| TGG GTG GCC CTT ACT CCC ACC GTG GCG GCG CCT TAC GTT GGT GCT CCG | 384 |
| Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro |     |

| 115                                                             | 120 | 125 |     |
|-----------------------------------------------------------------|-----|-----|-----|
| CTA GAA TCC CTC CGG AGT CAT GTG GAT CTG ATG GTA GGT GCT GCT ACT |     |     | 432 |
| Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr |     |     |     |
| 130                                                             | 135 | 140 |     |
| GTG TGC TCC GCT CTT TAC ATC GGG GAC CTG TGC GGT GGC GTA TTT TTG |     |     | 480 |
| Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu |     |     |     |
| 145                                                             | 150 | 155 | 160 |
| GTT GGT CAG ATG TTT TCT TTC CAG CCG CGA CGC CAC TGG ACC ACG CAG |     |     | 528 |
| Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln |     |     |     |
| 165                                                             | 170 | 175 |     |
| GAC TGC AAT TGT TCT ATC TAC GCG GGG CAC GTT ACG GGC CAC AGG ATG |     |     | 576 |
| Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met |     |     |     |
| 180                                                             | 185 | 190 |     |
| GCA                                                             |     |     | 579 |
| Ala                                                             |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

|                                                                 |     |     |    |
|-----------------------------------------------------------------|-----|-----|----|
| Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala |     |     |    |
| 1                                                               | 5   | 10  | 15 |
| Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val |     |     |    |
| 20                                                              | 25  | 30  |    |
| Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe |     |     |    |
| 35                                                              | 40  | 45  |    |
| Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser |     |     |    |
| 50                                                              | 55  | 60  |    |
| Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp |     |     |    |
| 65                                                              | 70  | 75  | 80 |
| Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His |     |     |    |
| 85                                                              | 90  | 95  |    |
| Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys |     |     |    |
| 100                                                             | 105 | 110 |    |
| Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro |     |     |    |
| 115                                                             | 120 | 125 |    |
| Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr |     |     |    |
| 130                                                             | 135 | 140 |    |

Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu  
 145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met  
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Ala Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Ser Phe Trp His Phe Ser Arg Ala \* Leu Ser Arg Pro Arg  
 50 55 60  
 Leu Ser Thr Thr Gly Met Ser Arg Ala Ser Thr Thr Ser Pro Met Ile  
 65 70 75 80  
 Ala Arg Ile Pro Ala \* Cys Met Lys Pro Ile Thr Thr Ser Cys Thr  
 85 90 95  
 Tyr Gln Gly Ala Tyr Pro Ala \* Gly Pro Gly Thr Phe Arg Ala Ala  
 100 105 110  
 Gly Tyr Leu \* His Leu Leu Trp Leu Leu Pro Thr Ser Gly Leu Arg  
 115 120 125  
 Leu Arg Arg Tyr Gly Gly Met Trp Ile \* Trp Trp Val Gln Pro Pro  
 130 135 140  
 Phe Ala Leu Pro Ser Thr Ser Glu Thr Ser Val Glu Val Ser Ser \*  
 145 150 155 160  
 Trp Asp Arg Cys Ser Pro Ser Ser Arg Ala Ala Thr Gly Pro Leu Arg  
 165 170 175  
 Thr Ala Thr Ala Pro Phe Thr Ser Ala Thr Ser Gln Ala Thr Glu Trp

190

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ACT | TGC | GGC | TTT | GCC | GAC | CTC | ATG | GGA | TAC | ATC | CCG | CTC | GTA | GGC | GCC | 48  |
| Thr | Cys | Gly | Phe | Ala | Asp | Leu | Met | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| CCC | GTG | GGT | GGC | GTC | GCC | AGA | GCC | CTG | GAA | CAT | GGT | GTT | AGG | GCT | GTG | 96  |
| Pro | Val | Gly | Gly | Val | Ala | Arg | Ala | Leu | Glu | His | Gly | Val | Arg | Ala | Val |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| GAG | GAC | GGC | ATC | AAT | TAT | GCA | ACA | GGG | AAT | CTC | CCC | GGT | TGC | TCT | TTC | 144 |
| Glu | Asp | Gly | Ile | Asn | Tyr | Ala | Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| TCT | ATC | TAC | CTC | TTG | GCA | CTT | CTC | TCG | TGC | CTG | ACT | GTT | CCC | ACC | TCG | 192 |
| Ser | Ile | Tyr | Leu | Leu | Ala | Leu | Leu | Ser | Cys | Leu | Thr | Val | Pro | Thr | Ser |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| GCC | ATC | CAC | TAT | CGC | AAT | GCC | TCG | GGC | GTC | TAC | CAC | GTC | ACC | AAT | GAC | 240 |
| Ala | Ile | His | Tyr | Arg | Asn | Ala | Ser | Gly | Val | Tyr | His | Val | Thr | Asn | Asp |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| TGC | CCG | AAC | TCG | AGC | ATA | GTG | TAC | GAG | GCC | GAC | CAC | CAC | ATC | CTA | CAC | 288 |
| Cys | Pro | Asn | Ser | Ser | Ile | Val | Tyr | Glu | Ala | Asp | His | His | Ile | Leu | His |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| CTT | CCA | GGG | TGC | TTA | CCC | TGT | GTG | AGG | GTT | GGG | AAT | CAG | TCA | CGT | TGT | 336 |
| Leu | Pro | Gly | Cys | Leu | Pro | Cys | Val | Arg | Val | Gly | Asn | Gln | Ser | Arg | Cys |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| TGG | GTG | GCC | CTC | TCT | CCC | ACC | GTG | GCG | GCG | CCT | TAC | ATC | GGT | GCT | CCA | 384 |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro |     |
| 115 120 125                                                     |     |
| GTT GAA TCC TTC CGG AGA CAC GTG GAC ATG ATG GTG GGC GCT GCT ACT | 432 |
| Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr |     |
| 130 135 140                                                     |     |
| GTG TGC TCC GCT CTC TAT ATT GGG GAC TTG TGT GGT GGC GTA TTC TTG | 480 |
| Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu |     |
| 145 150 155 160                                                 |     |
| GTT GGT CAG ATG TTT TCT TTC CGG CCA CGA CGC CAC TGG ACT ACG CAG | 528 |
| Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln |     |
| 165 170 175                                                     |     |
| GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC ATC ACT GGC CAC GGA ATG | 576 |
| Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met |     |
| 180 185 190                                                     |     |
| GCA                                                             | 579 |
| Ala                                                             |     |

## (2) INFORMATION FOR SEQ ID NO: 186:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala |  |
| 1 5 10 15                                                       |  |
| Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val |  |
| 20 25 30                                                        |  |
| Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe |  |
| 35 40 45                                                        |  |
| Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser |  |
| 50 55 60                                                        |  |
| Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp |  |
| 65 70 75 80                                                     |  |
| Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His |  |
| 85 90 95                                                        |  |
| Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys |  |
| 100 105 110                                                     |  |
| Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro |  |
| 115 120 125                                                     |  |



Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr  
 130 135 140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
 145 150 155 160

Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met  
 180 185 190

Ala

## (2) INFORMATION FOR SEQ ID NO: 187:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC | 48  |
| Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala |     |
| 1 5 10 15                                                       |     |
| CCT GTG GGT GGC GTC GCC AGG GCC CTG GCA CAC GGT GTT AGG GCT GTG | 96  |
| Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val |     |
| 20 25 30                                                        |     |
| GAG GAC GGG ATC AAT TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC | 144 |
| Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe |     |
| 35 40 45                                                        |     |
| TCT ATC TTC CTC TTG GCA CTT CTT TCG TGC CTG ACT GTT CCC ACC TCG | 192 |
| Ser Ile Phe Leu Leu Ala Leu Ser Cys Leu Thr Val Pro Thr Ser     |     |
| 50 55 60                                                        |     |
| GCC GTC AAC TAT CGC AAT GCC TCG GGC ATC TAT CAC ATC ACC AAT GAC | 240 |

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
65 70 75 80

TGC CCG AAC TCG AGC ATA GTG TAC GAG ACC GAG CAC CAC ATC CTA CAC 288  
Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His  
85 90 95

CTC CCA GGG TGT TTA CCC TGC GTG AGG GTT GGG AAT CAG TCA CGC TGC 336  
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys  
100 105 110

TGG GTG GCC CTC ACT CCC ACC GTG GCG GCG CCT TAC ATC GGC GCT CCG 384  
Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro  
115 120 125

CTT GAA TCC CTC CGG AGT CAT GTG GAT CTG ATG GTA GGT GCC GCT ACT 432  
Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr  
130 135 140

GCG TGC TCC GCT CTT TAC ATC GGA GAC CTG TGC GGT GGC GTA TTT TTG 480  
Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
145 150 155 160

GTT GGT CAG ATG TTC TCT TTC CAG CCG CGG CGC CAC TGG ACT ACG CAG 528  
Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
165 170 175

GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC GTT ACG GGC CAC AGG ATG 576  
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met  
180 185 190

GCA 579  
Ala

## (2) INFORMATION FOR SEQ ID NO: 188:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 193 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser  
50 55 60

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His  
85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys  
100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro  
115 120 125

Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr  
130 135 140

Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
145 150 155 160

Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met  
180 185 190

Ala

## (2) INFORMATION FOR SEQ ID NO: 189:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

ACG TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC  
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
1 5 10 15

48

CCC GTT GGG GGC GTC GCC AGG GCC CTG GCG CAT GGC GTC AGG GCT GTG 96  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
                     20                    25                    30

GAG GAC GGG ATT AAC TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC 144  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
                     35                    40                    45

TCT ATC TTC CTC CTG GCA CTT CTT TCG TGC CTC ACT GTC CCA GCG TCA 192  
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
                     50                    55                    60

GCT GAG CAC TAC CGG AAT GCT TCG GGC ATC TAT CAC ATC ACC AAT GAC 240  
 Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
                     65                    70                    75                    80

TGT CCG AAT TCC AGC GTA GTC TAT GAA ACT GAC CAC CAT ATA TTG CAC 288  
 Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His  
                     85                    90                    95

TTG CCG GGG TGC GTA CCC TGC GTG AGG GCC GGG AAC GTG TCT CGT TGC 336  
 Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys  
                     100                    105                    110

TGG ACG CCG GTA ACA CCT ACG GTG GCT GCC GTA TCC ATG GAC GCT CCG 384  
 Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro  
                     115                    120                    125

CTC GAG TCC TTC CGG CGG CAT GTG GAC CTA ATG GTA GGT GCG GCC ACC 432  
 Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
                     130                    135                    140

GTG TGT TCT GTC CTC TAT GTT GGA GAC CTC TGT GGA GGT GCT TTC CTA 480  
 Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu  
                     145                    150                    155                    160

GTG GGG CAG ATG TTC ACC TTC CAG CCG CGT CGC CAC TGG ACC ACG CAG 528  
 Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
                     165                    170                    175

GAT TGT AAT TGC TCC ATC TAT ACT GGC CAT ATC ACC GGC CAC AGG ATG 576  
 Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met  
                     180                    185                    190

GCG 579  
 Ala

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His  
 85 90 95  
 Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys  
 100 105 110  
 Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro  
 115 120 125  
 Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140  
 Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met  
 180 185 190  
 Ala

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 1..289

## (ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC   | 48  |
| Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn   |     |
| 1 5 10 15                                                         |     |
| CGC CGC CCC ATG GAC GTT AAG TTC CCG GGC GGT GGC CAG ATC GTT GGT   | 96  |
| Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly   |     |
| 20 25 30                                                          |     |
| GGA GTT TAC TTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG   | 144 |
| Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala   |     |
| 35 40 45                                                          |     |
| ACT AGG AAG ACT TCG GAG CGG TCG CAA CCT CGT GGG AGA CGT CAG CCT   | 192 |
| Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro   |     |
| 50 55 60                                                          |     |
| ATC CCC AAG GCA CGT CGA TCT GAG GGA AGG TCC TGG GCT CAG CCC GGG   | 240 |
| Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly   |     |
| 65 70 75 80                                                       |     |
| TAC CCA TGG CCT CTT TAC GGT AAT GAG GGT TGT GGG TGG GCA GGA TGG G | 289 |
| Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp   |     |
| 85 90 95                                                          |     |

(2) INFORMATION FOR SEQ ID NO: 192:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn |  |
| 1 5 10 15                                                       |  |
| Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly |  |
| 20 25 30                                                        |  |
| Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala |  |
| 35 40 45                                                        |  |
| Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro |  |
| 50 55 60                                                        |  |
| Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly |  |

65

70

75

80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp  
                     85                    90                    95

## (2) INFORMATION FOR SEQ ID NO: 193:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..498

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..495

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

|                                                                      |     |
|----------------------------------------------------------------------|-----|
| ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC      | 48  |
| Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn      |     |
| 1                    5                    10                    15   |     |
| CGC CGC CCT ATG GAC GTA AAG TTC CCG GGC GGT GGA CAG ATC GTT GGC      | 96  |
| Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly      |     |
| 20                    25                    30                       |     |
| GGA GTT TAC TTG TTG CCG CGC AGG GGC CCC CGG TTG GGT GTG CGC GCG      | 144 |
| Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala      |     |
| 35                    40                    45                       |     |
| ACT CGG AAG ACT TCG GAG CGG TCG CAA CCT CGT GGC AGG CGT CAA CCT      | 192 |
| Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro      |     |
| 50                    55                    60                       |     |
| ATC CCC AAG GCG CGC CGG TCC GAG GGC AGG TCC TGG GCG CAA GCC GGG      | 240 |
| Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Ala Gly      |     |
| 65                    70                    75                    80 |     |
| TAC CCC TGG CCC CTC TAT GGC AAT GAG GGC TGT GGG TGG GCA GGG TGG      | 288 |
| Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp      |     |
| 85                    90                    95                       |     |
| CTC CTG TCT CCT CGC GGC TCT CGG CCA TCT TGG GGC CCA AAT GAT CCC      | 336 |

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro  
 100 105 110  
 CGG CGG AGA TCG CGC AAT CTG GGT AAG GTC ATC GAT ACC CTG ACG TGC 384  
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC CCC GTC 432  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val  
 130 135 140  
 GGG GGC GTC GCC AGG GCC CTG GCG CAT GGC GTC AGG GCT GTG GAG GAC 480  
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp  
 145 150 155 160  
 GGG ATT AAC TAT CGA CAG 498  
 Gly Ile Asn Tyr Arg Gln  
 165

## (2) INFORMATION FOR SEQ ID NO: 194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
 1 5 10 15  
 Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
 20 25 30  
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala  
 35 40 45  
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60  
 Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Ala Gly  
 65 70 75 80  
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp  
 85 90 95  
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro  
 100 105 110  
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val  
 130 135 140



Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp  
 145 150 155 160

Gly Ile Asn Tyr Arg Gln  
 165

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ACG TGC GGA TTC GCC GAC CTC GTG GGG TAC ATC CCG CTC GTA GGC GGC | 48  |
| Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly |     |
| 1 5 10 15                                                       |     |
| CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAT GGT GTG AGG GTT CTT | 96  |
| Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu |     |
| 20 25 30                                                        |     |
| GAG GAC GGG GTG AAT TAT GCA ACA GGG AAT CTG CCT GGT TGC TCT TTC | 144 |
| Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe |     |
| 35 40 45                                                        |     |
| TCT ATC TTC ATT CTT GCA CTT CTC TCG TGC CTC ACT GTC CCG GCC TCT | 192 |
| Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser |     |
| 50 55 60                                                        |     |
| GCA GTT CCC TAC CGA AAT GCC TCT GGG ATC TAT CAT GTC ACC AAT GAT | 240 |
| Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp |     |
| 65 70 75 80                                                     |     |
| TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT GAT CTG ATC CTA CAC | 288 |
| Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His |     |
| 85 90 95                                                        |     |
| GCA CCT GGC TGC GTG CCT TGT GTC AGG AAA GAT AAT GTG AGT AGG TGC | 336 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| Ala | Pro | Gly | Cys | Val | Pro | Cys | Val | Arg | Lys | Asp | Asn | Val | Ser | Arg | Cys |  |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |     |
| TGG | GTC | CAA | ATT | ACC | CCC | ACG | CTG | TCA | GCC | CCG | AGC | TTC | GGA | GCA | GTC |  | 384 |
| Trp | Val | Gln | Ile | Thr | Pro | Thr | Leu | Ser | Ala | Pro | Ser | Phe | Gly | Ala | Val |  |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |     |
| ACG | GCT | CCC | CTT | CGG | AGA | GCC | GTT | GAT | TAC | TTG | GTG | GGA | GGG | GCT | GCC |  | 432 |
| Thr | Ala | Pro | Leu | Arg | Arg | Ala | Val | Asp | Tyr | Leu | Val | Gly | Gly | Ala | Ala |  |     |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |     |
| CTC | TGC | TCC | GCG | TTA | TAC | GTT | GGA | GAC | GCG | TGT | GGG | GCA | CTA | TTT | TTG |  | 480 |
| Leu | Cys | Ser | Ala | Leu | Tyr | Val | Gly | Asp | Ala | Cys | Gly | Ala | Leu | Phe | Leu |  |     |
|     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |     |
| GTA | GGC | CAA | ATG | TTC | ACC | TAT | AGG | CCT | CGC | CAG | CAT | GCT | ACG | GTG | CAG |  | 528 |
| Val | Gly | Gln | Met | Phe | Thr | Tyr | Arg | Pro | Arg | Gln | His | Ala | Thr | Val | Gln |  |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |     |
| GAC | TGC | AAC | TGT | TCC | ATC | TAC | AGT | GGC | CAC | GTC | ACC | GGC | CAT | CAG | ATG |  | 576 |
| Asp | Cys | Asn | Cys | Ser | Ile | Tyr | Ser | Gly | His | Val | Thr | Gly | His | Gln | Met |  |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |     |
| GCA |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  | 579 |
| Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |     |

## (2) INFORMATION FOR SEQ ID NO: 196:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Thr | Cys | Gly | Phe | Ala | Asp | Leu | Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Gly |  |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |  |
| Pro | Val | Gly | Gly | Val | Ala | Arg | Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu |  |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |  |
| Glu | Asp | Gly | Val | Asn | Tyr | Ala | Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |  |
| Ser | Ile | Phe | Ile | Leu | Ala | Leu | Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser |  |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Ala | Val | Pro | Tyr | Arg | Asn | Ala | Ser | Gly | Ile | Tyr | His | Val | Thr | Asn | Asp |  |  |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |  |
| Cys | Pro | Asn | Ser | Ser | Ile | Val | Tyr | Glu | Ala | Asp | Asp | Leu | Ile | Leu | His |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |  |
| Ala | Pro | Gly | Cys | Val | Pro | Cys | Val | Arg | Lys | Asp | Asn | Val | Ser | Arg | Cys |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |  |

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val  
 115 120 125

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala  
 130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu  
 145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln  
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met  
 180 185 190

Ala

## (2) INFORMATION FOR SEQ ID NO: 197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC | 48  |
| Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala |     |
| 1 5 10 15                                                       |     |
| CCC GTG GGT GGC GTC GCC AGA GCC CTG GAA CAT GGT GTT AGG GCT GTG | 96  |
| Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val |     |
| 20 25 30                                                        |     |
| GAG GAC GGC ATC AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTC | 144 |
| Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe |     |
| 35 40 45                                                        |     |
| TCT ATC TAC CTC TTG GCA CTT CTC TCG TGC CTG ACT GTT CCC ACC TCG | 192 |

Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser  
50 55 60

GCC ATC CAC TAT CGC AAT GCC TCG GGC GTC TAC CAC GTC ACC AAT GAC 240  
Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp  
65 70 75 80

TGC CCG AAC TCG AGC ATA GTG TAC GAG GCC GAC CAC CAC ATC CTA CAC 288  
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His  
85 90 95

CTT CCA GGG TGC TTA CCC TGT GTG AGG GTT GGG AAT CAG TCA CGT TGT 336  
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys  
100 105 110

TGG GTG GCC CTC TCT CCC ACC GTG GCG GCG CCT TAC ATC GGT GCT CCA 384  
Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro  
115 120 125

GTT GAA TCC TTC CGG AGA CAC GTG GAC ATG ATG GTG GGC GCT GCT ACT 432  
Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr  
130 135 140

GTG TGC TCC GCT CTC TAT ATT GGG GAC TTG TGT GGT GGC GTA TTC TTG 480  
Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
145 150 155 160

GTT GGT CAG ATG TTT TCT TTC CGG CCA CGA CGC CAC TGG ACT ACG CAG 528  
Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln  
165 170 175

GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC ATC ACT GGC CAC GGA ATG 576  
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met  
180 185 190

GCA 579  
Ala

## (2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 193 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val  
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe

45

Ala

|                                                                                                                                                     |     |
|-----------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| A TCA CCA CCG GAG CTT CTA TCA CAT ACT CCA CTT ACG GCA AGT TCC<br>Ser Pro Pro Glu Leu Leu Ser His Thr Pro Leu Thr Ala Ser Ser<br>1 5 10 15           | 46  |
| TTG CTG ATG GAG GGT GTT CAG GCG GCG CGC ATG ACG TGA TCA TAT GCG<br>Leu Leu Met Glu Gly Val Gln Ala Ala Arg Met Thr * Ser Tyr Ala<br>20 25 30        | 94  |
| ACG AGT GCC ATT CCC AGG ACG CCA CCA CCA TTC TTG GGA TAG GCA CTG<br>Thr Ser Ala Ile Pro Arg Thr Pro Pro Pro Phe Leu Gly * Ala Leu<br>35 40 45        | 142 |
| TCC TTG ACC AGG CAG AGA CGG CTG GAG CTA GGC TCG TCG TCT TGG CCA<br>Ser Leu Thr Arg Gln Arg Arg Leu Glu Leu Gly Ser Ser Ser Trp Pro<br>50 55 60      | 190 |
| CGG CCA CCC CTC CCG GCA GTG TGA CAA CGC CCC ACC CCA ACA TCG AGG<br>Arg Pro Pro Leu Pro Ala Val * Gln Arg Pro Thr Pro Thr Ser Arg<br>65 70 75        | 238 |
| AAG TGG CCC TGC CTC AGG AGG GGG AGG TTC CCT TCT ACG GCA GAG CCA<br>Lys Trp Pro Cys Leu Arg Arg Gly Arg Phe Pro Ser Thr Ala Glu Pro<br>80 85 90 95   | 286 |
| TTC CCC TTG CTT TTA TAA AGG GTG GTA GGC ATC TCA TCT TCT GCC ATT<br>Phe Pro Leu Leu Leu * Arg Val Val Gly Ile Ser Ser Ser Ala Ile<br>100 105 110     | 334 |
| CCA AGA AAA AAT GTG ATG AAC TCG CCA AGC AAC TGA CCA GCC TGG GCG<br>Pro Arg Lys Asn Val Met Asn Ser Pro Ser Asn * Pro Ala Trp Ala<br>115 120 125     | 382 |
| TGA ACG CCG TGG CAT ATT ATA GAG GTC TAG ACG TCG CCG TCA TAC CCA<br>* Thr Pro Trp His Ile Ile Glu Val * Thr Ser Pro Ser Tyr Pro<br>130 135 140       | 430 |
| CAA CAG GAG ACG TGG TCG TGT GCA GCA CCG ACG CGC TCA TGA CGG GAT<br>Gln Gln Glu Thr Trp Ser Cys Ala Ala Pro Thr Arg Ser * Arg Asp<br>145 150 155     | 478 |
| TCA CCG GCG ACT TTG ATT CTG TCA TAG ACT GCA ACT CCG CCG TCA CTC<br>Ser Pro Ala Thr Leu Ile Leu Ser * Thr Ala Thr Pro Pro Ser Leu<br>160 165 170 175 | 526 |
| AGA CGG TGG ACT TCA GTC TGG ATC CCA CTT TTA CCA TTG AGA CTA CCA<br>Arg Arg Trp Thr Ser Val Trp Ile Pro Leu Leu Pro Leu Arg Leu Pro<br>180 185 190   | 574 |
| CAG TGC CCC AGG ACG CAG TGT CCA GAA GCC AGC GTT GGG GCC GCA CGG<br>Gln Cys Pro Arg Thr Gln Cys Pro Glu Ala Ser Val Gly Ala Ala Arg<br>195 200 205   | 622 |
| GGA GAG GTA GGC ACG GCA TAT ACC GGT ATG TCT CGG CTG GAG AGA GAC<br>Gly Glu Val Gly Thr Ala Tyr Thr Gly Met Ser Arg Leu Glu Arg Asp<br>210 215 220   | 670 |
| CGT CTG GCA TGT TCG ACT CCG TGG TGC TCT GTG AGT GCT ACG ATG CCG<br>Arg Leu Ala Cys Ser Thr Pro Trp Cys Ser Val Ser Ala Thr Met Pro                  | 718 |

| 225                                                                                                                                                   | 230 | 235 |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|------|
| GAT GTG CAT GGT ACG ATC TGA CTC CTG CCG AGA CTA CCG TGA GGT TGC<br>Asp Val His Gly Thr Ile * Leu Leu Pro Arg Leu Pro * Gly Cys<br>240 245 250 255     |     |     | 766  |
| GCG CTT ACT AAA CAC CCC CGG GCT CCC TGT CTG TCA GGA CCA TTT GGA<br>Ala Leu Thr Lys His Pro Arg Ala Pro Cys Leu Ser Gly Pro Phe Gly<br>260 265 270     |     |     | 814  |
| ATT CTG GGA GGG GGT GTT CAC GGG GCT CAC TAA CAT CGA CGC TCA CAT<br>Ile Leu Gly Gly Gly Val His Gly Ala His * His Arg Arg Ser His<br>275 280 285       |     |     | 862  |
| GCT GTC ACA GAC CAA ACA GGG TGG GGA GAA TTT CCC ATA CCT TGT AGC<br>Ala Val Thr Asp Gln Thr Gly Trp Gly Glu Phe Pro Ile Pro Cys Ser<br>290 295 300     |     |     | 910  |
| GTA CCA AGC AAC AGT CTG TGT TCG CGC GAA AGC GCC CCC CCC CAG CTG<br>Val Pro Ser Asn Ser Leu Cys Ser Arg Glu Ser Ala Pro Pro Gln Leu<br>305 310 315     |     |     | 958  |
| GGA CAC AAT GTG GAA ATG CAT GCT CCG TCT CAA ACC GAC TTA ACT GGC<br>Gly His Asn Val Glu Met His Ala Pro Ser Gln Thr Asp Leu Thr Gly<br>320 325 330 335 |     |     | 1006 |
| CCT ACT CCC CTC TTG TAC AGG CTG GGG CCC GTC CAG AAT GAG ATC ACA<br>Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile Thr<br>340 345 350     |     |     | 1054 |
| CTG ACG CAC CCC ATC ACC AAG TAC ATT ATG GCT TGC ATG TCT GCG GAC<br>Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp<br>355 360 365     |     |     | 1102 |
| TTG GAG GTC ATT ACC AGC ACT TGG GTT CTG GTG GGG GGC GTT GTG GCG<br>Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val Ala<br>370 375 380     |     |     | 1150 |
| GCC CTG GCG GCC TAC TGC TTG ACG GTG GGT TCG GTA GCC ATA GTC GGT<br>Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val Gly<br>385 390 395     |     |     | 1198 |
| AGG ATC ATC CTC TCT GGG AAA CCT GCC ATC ATT CCC GAT AGG GAG GTA<br>Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val<br>400 405 410 415 |     |     | 1246 |
| TTA TAC CAG CAA TTT GAT GAG ATG GAG GAG TGC TCG GCC TCG TTG CCC<br>Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu Pro<br>420 425 430     |     |     | 1294 |
| TAT ATG GAC GAA ACA CGT GCC ATT GCC GGA CAA TTC AAA GAG AAA GTG<br>Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys Val<br>435 440 445     |     |     | 1342 |
| CTC GGC TTC ATC AGC ACG ACC GGC CAG AAG GCT GAA ACT CTG AAG CCG<br>Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys Pro<br>450 455 460     |     |     | 1390 |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| GCA GCC ACG TCT GTG TGG AAC AAG GCT GAG CAG TTC TGG CCA CAT ACA | 1438 |
| Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Pro His Thr |      |
| 465 470 475                                                     |      |

|                                            |      |
|--------------------------------------------|------|
| TGT GGA ACT TCA TCA GTG GGA TAC AAT AAT AG | 1470 |
| Cys Gly Thr Ser Ser Val Gly Tyr Asn Asn    |      |
| 480 485                                    |      |

## (2) INFORMATION FOR SEQ ID NO: 197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1485

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| TGTGCCAGGA CCATCACCAC CGGAGCTTCT ATCACATACT CCACTTACGG CAAGTTCCTT   | 60  |
| GCTGATGGAG GGTGTTTCAGG CGGCGCGCAT GACGTGATCA TATGCGACGA GTGCCATTCC  | 120 |
| CAGGACGCCA CCACCATTCT TGGGATAGGC ACTGTCCTTG ACCAGGCAGA GACGGCTGGA   | 180 |
| GCTAGGCTCG TCGTCTTGGC CACGGCCACC CCTCCCGGCA GTGTGACAAC GCCCCACCCC   | 240 |
| AACATCGAGG AAGTGGCCCT GCCTCAGGAG GGGGAGGTTT CCTTCTACGG CAGAGCCATT   | 300 |
| CCCCTTGCTT TTATAAAGGG TGGTAGGCAT CTCATCTTCT GCCATTCCAA GAAAAAATGT   | 360 |
| GATGAACTCG CCAAGCAACT GACCAGCCTG GCGGTGAACG CCGTGGCATA TTATAGAGGT   | 420 |
| CTAGACGTCG CCGTCATACC CACAACAGGA GACGTGGTCG TGTGCAGCAC CGACGCGCTC   | 480 |
| ATGACGGGAT TCACCGGCGA CTTTGATTCT GTCATAGACT GCAACTCCGC CGTCACTCAG   | 540 |
| ACGGTGGACT TCAGTCTGGA TCCCACTTTT ACCATTGAGA CTACCACAGT GCCCCAGGAC   | 600 |
| GCAGTGTCCA GAAGCCAGCG TTGGGGCCGC ACGGGGAGAG GTAGGCACGG CATATACCGG   | 660 |
| TATGTCTCGG CTGGAGAGAG ACCGTCTGGC ATGTTTCTGACT CCGTGGTGCT CTGTGAGTGC | 720 |
| TACGATGCCG GATGTGCATG GTACGATCTG ACTCCTGCCG AGACTACCGT GAGGTTGCGC   | 780 |
| GCTTACNTAA ACACCCCCCG GCTCCCTGTC TGTCAGGACC ATTTGGAATT CTGGGAGGGG   | 840 |
| GTGTTACCGG GGCTCACTAA CATCGACGCT CACATGCTGT CACAGACCAA ACAGGGTGGG   | 900 |
| GAGAATTTCC CATACCTTGT AGCGTACCAA GCAACAGTCT GTGTTTCGCGC GAAAGCGCCC  | 960 |



```

CCCCCAGCT GGGACACAAT GTGGAAATGC ATGCTCCGTC TCAAACCGAC NTTAACTGGC 1020
CCTACTCCCC TCTTGTACAG GCTGGGGCCC GTCCAGAATG AGATCACACT GACGCACCCC 1080
ATCACCAAGT ACATTATGGC TTGCATGTCT GCGGACTTGG AGGTCATTAC CAGCACTTGG 1140
GTTCTGGTGG GGGGCGTTGT GGCGGCCCTG GCGGCCTACT GCTTGACGGT GGGTTCGGTA 1200
GCCATAGTCG GTAGGATCAT CCTCTCTGGG AAACCTGCCA TCATTCCCGA TAGGGAGGTA 1260
TTATACCAGC AATTTGATGA GATGGAGGAG TGCTCGGCCT CGTTGCCCTA TATGGACGAA 1320
ACACGTGCCA TTGCCGGACA ATTCAAAGAG AAAGTGCTCG GCTTCATCAG CACGACCGGC 1380
CAGAAGGCTG AAACCTTGAA GCCGGCAGCC ACGTCTGTGT GGAACAAGGC TGAGCAGTTC 1440
TGGNCCACAT ACATGTGGAA CTTTCATCAGT GGGATACAAT AATAG 1485

```

## (2) INFORMATION FOR SEQ ID NO: 198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

```

Cys Ala Arg Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr
1 5 10 15
Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala His Asp Val
 20 25 30
Ile Ile Cys Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly
 35 40 45
Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val
 50 55 60
Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro
 65 70 75 80
Asn Ile Glu Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr
 85 90 95
Gly Arg Ala Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile
 100 105 110
Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr
 115 120 125
Ser Leu Gly Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala
 130 135 140

```

Val Ile Pro Thr Thr Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu  
 145 150 155 160  
 Met Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser  
 165 170 175  
 Ala Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile  
 180 185 190  
 Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Trp  
 195 200 205  
 Gly Arg Thr Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala  
 210 215 220  
 Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Val Val Leu Cys Glu Cys  
 225 230 235 240  
 Tyr Asp Ala Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr  
 245 250 255  
 Val Arg Leu Arg Ala Tyr Xaa Asn Thr Pro Gly Leu Pro Val Cys Gln  
 260 265 270  
 Asp His Leu Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile  
 275 280 285  
 Asp Ala His Met Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Phe Pro  
 290 295 300  
 Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro  
 305 310 315 320  
 Pro Pro Ser Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro  
 325 330 335  
 Xaa Leu Thr Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln  
 340 345 350  
 Asn Glu Ile Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys  
 355 360 365  
 Met Ser Ala Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly  
 370 375 380  
 Gly Val Val Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val  
 385 390 395 400  
 Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro  
 405 410 415  
 Asp Arg Glu Val Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser  
 420 425 430  
 Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe  
 435 440 445

Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu  
450 455 460

Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe  
465 470 475 480

Trp Xaa Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TGTGCCAGGA CCATCACCAC CGGAGCTTCT ATCACATACT CCACTTACGG CAAGTTCCTT  | 60  |
| GCTGATGGAG GGTGTTTCAGG CGGCGCGTAT GACGTGATCA TATGCGACGA GTGCCATTCC | 120 |
| CAGGACGCCA CCACCATTCT TGGGATAGGC ACTGTCCTTG ACCAGGCAGA GACGGCTGGA  | 180 |
| GCTAGGCTCG TCGTCTTGGC CACGGCCACC CCTCCCGGCA GTGTGACAAC GCCCCACCCC  | 240 |
| AACATCGAGG AAGTGGCCCT GCCTCAGGAG GGGGAGGTTT CTTTCTACGG CAGAGCCATT  | 300 |
| CCCCTTGCTT TTATAAAGGG TGGTAGGCAT CTCATCTTCT GCCATTCCAA GAAAAAATGT  | 360 |
| GATGAACCTG CCAAGCAACT GACCAGCCTG GCGTGAACG CCGTGGCATA TTATAGAGGT   | 420 |
| CTAGACGTCG CCGTCATCCC CACAGCAGGA GACGTGGTCG TGTGCAGCAC CGACGCGCTC  | 480 |
| ATGACGGGAT TCACCGGCGA CTTTGATTCT GTCATAGACT GCAACTCCGC CGTCACTCAG  | 540 |
| ACGGTGGACT TCAGTCTGGA TCCCACTTTT ACCATTGAGA CTACCACAGT GCCCCAGGAC  | 600 |
| GCAGTGTCCA GAAGCCAGCG TAGGGGCCGC ACGGGGAGAG GTAGGCACGG CATATACCGG  | 660 |
| TATGTCTCGG CTGGAGAGAG ACCNTCTGAC ATGTTTCGACT CCGTGGTGCT CTGTGAGTGC | 720 |
| TACGATGCCG GATGTGCGTG GTATGATCTG ACTCCTGCCG AGACTACCGT GAGGTTGCGC  | 780 |
| GCTTACATAA ACACCCCCGG GCTCCCTGTC TGTCAGGACC ATTTGGAATT CTGGGAGGGG  | 840 |
| GTGTTTCACG GGCTCACTAA CATCGACGCT CACATGCTGT CACAGACCAA ACAGGGTGGG  | 900 |
| GAGAATTTNC CATACTTGT AGCGTACCAA GCAACAGTCT GTGTTGCGCG GAAAGCGCCC   | 960 |

```

CCCCCAGCT GGGACACAAT GTGGAAATGC ATGCTCCGTC TCAAACCGAC TTAACTGGC 1020
CCTACTCCCC TCTTGTACAG GCTGGGGCCC GTCCAGANTG AGATCACACT GACGCACCCC 1080
ATCACCAAGT ACATTATGGC TTGCATGTCT GCGGACTTGG AGGTCATTAC CANCACTTGG 1140
GTTCTGGTGG GGGGCGTTGT GCGGGCCCTG GCGGCCTACT GCTTGACGGT GGGTTCGGTA 1200
GCCATAGTCG GTAGGATCAT CCTCTCTGGG AAACCTGCCA TCATTCCCGA TAGGGAGGCA 1260
TTATACCAGC AATTTGATGA GATGGAGGAG TGCTCGGCCT CGTTGCCCTA TATGGACGAG 1320
ACACGTGCCA TTGCCGGACA ATTCAAAGAG AAAGTGCTCG GCTTCATCAG CACGACCGGC 1380
CAGAAGGCTG AAACTCTGAA GCCGGCAGCC ACGTCTGTGT GGAACAAGGC TGAGCAGTTC 1440
TGGGCCACAT ACATGTGGAA CTTTCATCAGC GGGATACAAT AATAG 1485

```

## (2) INFORMATION FOR SEQ ID NO: 200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

```

Cys Ala Arg Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr
1 5 10 15
Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val
20 25 30
Ile Ile Cys Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly
35 40 45
Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val
50 55 60
Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro
65 70 75 80
Asn Ile Glu Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr
85 90 95
Gly Arg Ala Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile
100 105 110
Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr
115 120 125

```

Ser Leu Gly Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala  
 130 135 140  
 Val Ile Pro Thr Ala Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu  
 145 150 155 160  
 Met Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser  
 165 170 175  
 Ala Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile  
 180 185 190  
 Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg  
 195 200 205  
 Gly Arg Thr Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala  
 210 215 220  
 Gly Glu Arg Xaa Ser Asp Met Phe Asp Ser Val Val Leu Cys Glu Cys  
 225 230 235 240  
 Tyr Asp Ala Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr  
 245 250 255  
 Val Arg Leu Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln  
 260 265 270  
 Asp His Leu Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile  
 275 280 285  
 Asp Ala His Met Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Xaa Pro  
 290 295 300  
 Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro  
 305 310 315 320  
 Pro Pro Ser Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro  
 325 330 335  
 Thr Leu Thr Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln  
 340 345 350  
 Xaa Glu Ile Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys  
 355 360 365  
 Met Ser Ala Asp Leu Glu Val Ile Thr Xaa Thr Trp Val Leu Val Gly  
 370 375 380  
 Gly Val Val Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val  
 385 390 395 400  
 Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro  
 405 410 415  
 Asp Arg Glu Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser  
 420 425 430  
 Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe

435

440

445

Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu  
 450 455 460

Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe  
 465 470 475 480

Trp Ala Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| C TCC ACT GTG ACT GAG AGA GAC ATC AGG GTC GAA GAA GAA GTC TAT   | 46  |
| Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr     |     |
| 1 5 10 15                                                       |     |
| CAG TGT TGT GAT CTG GAG CCC GAG GCC CGC AAG GTA ATA ACC GCC CTC | 94  |
| Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu |     |
| 20 25 30                                                        |     |
| ACG GAG AGA CTC TAC GTG GGC GGC CCT ATG TAC AAT AGC AAG GGA GAC | 142 |
| Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp |     |
| 35 40 45                                                        |     |
| CTT TGC GGG TAT CGC AGG TGC CGC GCA AGC GGC GTA TAT ACC ACC AGC | 190 |
| Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser |     |
| 50 55 60                                                        |     |
| TTC GGG AAC ACA CTG ACG TGC TAC CTT AAA GCC TCA GCA GCC ATC AGG | 238 |
| Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg |     |
| 65 70 75                                                        |     |
| GCT GCG GGG CTG AAG GAC TGC ACC ATG CTG GTT TGC GGT GAC GAC TTA | 286 |
| Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu |     |
| 80 85 90 95                                                     |     |

GTC GTG ATC GCT GAA AGC GGT GGC GTC GAG GAG GAC AAG CGA GCC CTC 334  
 Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu  
                   100                  105                  110

GGA GCT 340  
 Gly Ala

(2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln  
   1                  5                  10                  15  
 Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr  
                   20                  25                  30  
 Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu  
                   35                  40                  45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
                   50                  55                  60  
 Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala  
   65                  70                  75                  80  
 Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
                   85                  90                  95  
 Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu Gly  
                   100                  105                  110  
 Ala

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 2..340

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
(B) LOCATION: 2..337

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| C TCC ACA GTG ACT GAA AGA GAC ATC AGG GTC GAG GAA GAG GTC TAC   | 46  |
| Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr     |     |
| 1 5 10 15                                                       |     |
| CAG TGT TGT GAC CTG GAG CCT GAA ACC CGC AAG GTA ATA TCT GCC CTC | 94  |
| Gln Cys Cys Asp Leu Glu Pro Glu Thr Arg Lys Val Ile Ser Ala Leu |     |
| 20 25 30                                                        |     |
| ACT GAA AGA CTC TAT GTG GGC GGT CCC ATG CAC AAC AGC AGG GGA GAC | 142 |
| Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp |     |
| 35 40 45                                                        |     |
| CTA TGC GGG TAC CGT AGA TGC CGC GCG AGC GGC GTA TAC ACC ACA AGC | 190 |
| Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser |     |
| 50 55 60                                                        |     |
| TTC GGG AAC ACT CTG ACG TGC TTC CTC AAG GCC ACA GCG GCC ACC AAA | 238 |
| Phe Gly Asn Thr Leu Thr Cys Phe Leu Lys Ala Thr Ala Ala Thr Lys |     |
| 65 70 75                                                        |     |
| GCC GCT GGC CTA AAG GAC TGC ACC ATG TTG GTG TGT GGT GAC GAC TTA | 286 |
| Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu |     |
| 80 85 90 95                                                     |     |
| GTC GTT ATC GCC GAA AGC GAT GGT GTC GAA GAG GAC CGC CGA GCC CTC | 334 |
| Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Arg Arg Ala Leu |     |
| 100 105 110                                                     |     |
| GGA GCT                                                         | 340 |
| Gly Ala                                                         |     |

## (2) INFORMATION FOR SEQ ID NO: 204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

|                                                                 |
|-----------------------------------------------------------------|
| Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln |
| 1 5 10 15                                                       |







## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 2..337

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| C TCC ACG GTG ACT GAA AGG GAC ATT AGG GTC GAG GAA GAG ATC TAC   | 46  |
| Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Ile Tyr     |     |
| 1 5 10 15                                                       |     |
| CAG TGC TGT GAC CTG GAG CCC GAG GCA CGC AAG GTG ATA TCC GCT CTC | 94  |
| Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu |     |
| 20 25 30                                                        |     |
| ACA GAA AGA CTC TAC AAG GGC GGC CCC ATG TAT AAC AGC AAG GGG GAC | 142 |
| Thr Glu Arg Leu Tyr Lys Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp |     |
| 35 40 45                                                        |     |
| CTA TGC GGG CTT CGG AGG TGC CGC GCA AGC GGG GTA TAC ACC ACA AGC | 190 |
| Leu Cys Gly Leu Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser |     |
| 50 55 60                                                        |     |
| TTC GGG AAC ACG GTG ACA TGC TAC CTT AAA GCC ACA GCA GCC ACC AGG | 238 |
| Phe Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg |     |
| 65 70 75                                                        |     |
| GCT GCA GGG CTG AAA GAT TGC ACT ATG CTG GTA TGC GGT GAC GAC TTA | 286 |
| Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu |     |
| 80 85 90 95                                                     |     |
| GTC GTT ATT GCC GAA AGC GGT GGC GTG GAG GAG GAC GCC CGA GCC CTC | 334 |
| Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu |     |
| 100 105 110                                                     |     |
| CGA GCC                                                         | 340 |
| Arg Ala                                                         |     |

## (2) INFORMATION FOR SEQ ID NO: 208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln  
 1 5 10 15  
 Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr  
 20 25 30  
 Glu Arg Leu Tyr Lys Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu  
 35 40 45  
 Cys Gly Leu Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
 50 55 60  
 Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala  
 65 70 75 80  
 Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg  
 100 105 110  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..340

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

CCCCACCGTG ACNGAGAGGG ACNTCAGGGT CGAGGAAGAG GTCTATCAGT GCTGTAATCT 60  
 GGAGNCCGAT GNCCGCAAGG TCATCAACGC CCTCACAGAG AGACTCTACG TGGGCGGCCC 120

TATGCACAAC AGCAAGGGAG ACCTGTGTGG CATCCGTAGA TGCCGCGCGA GCGGCGTTTA 180  
 CACCACGAGC TTCGGAAACA CGCTGACTTG CTACCTCAAA GCCACAGCGG CCACCAGGGC 240  
 CGCGGGCTTG AAGGATTGCA CCATGCTGGT CTGCGGNGAC GACCTGGTTG TCATTGCTGA 300  
 GAGCATTGGC ATAGACGAGG ACAAGCAAGC CCTCCGNACT 340

## (2) INFORMATION FOR SEQ ID NO: 210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Pro | Thr | Val | Thr | Glu | Arg | Asp | Xaa | Arg | Val | Glu | Glu | Glu | Val | Tyr | Gln | 1   | 5   | 10  | 15 |
| Cys | Cys | Asn | Leu | Glu | Xaa | Asp | Xaa | Arg | Lys | Val | Ile | Asn | Ala | Leu | Thr | 20  | 25  | 30  |    |
| Glu | Arg | Leu | Tyr | Val | Gly | Gly | Pro | Met | His | Asn | Ser | Lys | Gly | Asp | Leu | 35  | 40  | 45  |    |
| Cys | Gly | Ile | Arg | Arg | Cys | Arg | Ala | Ser | Gly | Val | Tyr | Thr | Thr | Ser | Phe | 50  | 55  | 60  |    |
| Gly | Asn | Thr | Leu | Thr | Cys | Tyr | Leu | Lys | Ala | Thr | Ala | Ala | Thr | Arg | Ala | 65  | 70  | 75  | 80 |
| Ala | Gly | Leu | Lys | Asp | Cys | Thr | Met | Leu | Val | Cys | Gly | Asp | Asp | Leu | Val | 85  | 90  | 95  |    |
| Val | Ile | Ala | Glu | Ser | Ile | Gly | Ile | Asp | Glu | Asp | Lys | Gln | Ala | Leu | Arg | 100 | 105 | 110 |    |
| Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |

## (2) INFORMATION FOR SEQ ID NO: 211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| CTCGACTGTG | NCCGAGAGGG | ACATCAGGAC | AGAGGGAGAG | GTCTATCAGT | GTTGCGACCT  | 60  |
| GGAACCGGAA | GCCCCGAAGG | TAATCACCGC | CCTCACTGAG | AGACTCTATG | TGGGCGGACC  | 120 |
| CATGTTCAAC | AGCAAGGGAG | ACCTGTGCGG | ACAACGCCGG | TGCCGCGCAA | GCGGCGTGTT  | 180 |
| CACCACCAGC | TTCGGGAACA | CACTGACGTG | CTACCTTAAA | GCCACAGCTG | CTACTAGAGC  | 240 |
| AGCCGGCTTA | AAAGATTGCA | CCATGCTGGT | CTGCGGTGAC | GACTTAGTCG | TTATTTC CGA | 300 |
| GAGCGCCGGT | GTGGAGGAGG | ATCCCANAAC | CCNNCGACCN |            |             | 340 |

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212;

Ser Thr Val Xaa Glu Arg Asp Ile Arg Thr Glu Gly Glu Val Tyr Gln  
1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr  
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly Asp Leu  
35 40 45

Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Phe  
50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala

|                                                                 |     |    |     |    |  |     |
|-----------------------------------------------------------------|-----|----|-----|----|--|-----|
| 65                                                              |     | 70 |     | 75 |  | 80  |
| Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val |     |    |     |    |  |     |
|                                                                 | 85  |    |     | 90 |  | 95  |
| Val Ile Ser Glu Ser Ala Gly Val Glu Glu Asp Pro Xaa Thr Xaa Arg |     |    |     |    |  |     |
|                                                                 | 100 |    | 105 |    |  | 110 |
| Pro                                                             |     |    |     |    |  |     |

## (2) INFORMATION FOR SEQ ID NO: 213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2...340

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 2..337

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| C TCA ACA GTC ACC GAG AAC GAC ATC CGT GTT GAG GAG TCA ATT TAC   | 46  |
| Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr     |     |
| 1 5 10 15                                                       |     |
| CAA TGT TGT GAC TTG GCC CCC GAG GCC AGA CAG GCC ATA AAG TCG CTC | 94  |
| Gln Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser Leu |     |
| 20 25 30                                                        |     |
| ACA GAG CGG CTT TAT ATC GGG GGT CCC CTG ACT AAT TCA AAG GGG CAG | 142 |
| Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln |     |
| 35 40 45                                                        |     |
| AAC TGT GGC TAT CGC CGA TGC CGC GCA AGC GGC GTG CTG ACG ACC AGC | 190 |
| Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser |     |
| 50 55 60                                                        |     |
| TGC GGT AAT ACC CTT ACA TGT TAC CTA AAG GCC TCT GCA GCC TGT CGA | 238 |
| Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg |     |
| 65 70 75                                                        |     |
| GCT GCG AAG CTC CAG GAC TGC ACG ATG CTC GTG TGC GGG GAC GAC CTT | 286 |

Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu  
 80 85 90 95

GTC GTT ATC TGT GAA AGC GCG GGA ACC CAA GAG GAC GCG GCG AGC CTA 334  
 Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu  
 100 105 110

CGA GTC 340  
 Arg Val

## (2) INFORMATION FOR SEQ ID NO: 214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr Gln  
 1 5 10 15

Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser Leu Thr  
 20 25 30

Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn  
 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys  
 50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg Ala  
 65 70 75 80

Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95

Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu Arg  
 100 105 110

Val

## (2) INFORMATION FOR SEQ ID NO: 215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA



(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| C TCA ACC GTC ACG GAG AGG GAT ATA AGA ACA GAA GAA TCC ATA TAT   | 46  |
| Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr     |     |
| 1 5 10 15                                                       |     |
| CAA GCT TGT TCC CTG CCC CAA GAG GCC AGA ACT GTC ATA CAC TCG CTC | 94  |
| Gln Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu |     |
| 20 25 30                                                        |     |
| ACC GAG AGA CTC TAC GTG GGA GGG CCC ATG ATA AAC AGC AAA GGG CAA | 142 |
| Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Ile Asn Ser Lys Gly Gln |     |
| 35 40 45                                                        |     |
| TCC TGC GGT TAC AGG CGT TGC CGC GCA AGC GGT GTT TTC ACC ACC AGC | 190 |
| Ser Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser |     |
| 50 55 60                                                        |     |
| ATG GGG AAT ACC ATG ACG TGT TAC ATC AAA GCC CTT GCA GCG TGT AAA | 238 |
| Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys |     |
| 65 70 75                                                        |     |
| GCC GCA GGG ATC GTG GAC CCC GTC ATG CTG GTG TGT GGA GAC GAC CTG | 286 |
| Ala Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu |     |
| 80 85 90 95                                                     |     |
| GTC GTC ATC TCG GAG AGC CAG GGT AAC GAG GAG GAC GAG CGA AAC CTG | 334 |
| Val Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn Leu |     |
| 100 105 110                                                     |     |
| AGA GCT                                                         | 340 |
| Arg Ala                                                         |     |

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln  
 1 5 10 15  
 Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu Thr  
 20 25 30  
 Glu Arg Leu Tyr Val Gly Gly Pro Met Ile Asn Ser Lys Gly Gln Ser  
 35 40 45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met  
 50 55 60  
 Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys Ala  
 65 70 75 80  
 Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn Leu Arg  
 100 105 110  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 2..340

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

C TCG ACT GTC ACT GAA CAG GAC ATC AGG GTG GAA GAG GAG ATA TAT 46  
 Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr  
 1 5 10 15  
 CAA TGC TGC AAC CTT GAA CCG GAG GCC AGG AAA GTG ATC TCC TCC CTC 94  
 Gln Cys Cys Asn Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ser Leu

|                                                                 | 20  | 25  | 30  |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| ACG GAG CGG CTT TAC TGC GGA GGC CCT ATG TTT AAC AGC AAG GGG GCC |     |     |     | 142 |
| Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Ala |     |     |     |     |
|                                                                 | 35  | 40  | 45  |     |
| CAG TGT GGT TAT CGC CGT TGC CGT GCC AGT GGA GTT CTG CCT ACC AGC |     |     |     | 190 |
| Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser |     |     |     |     |
|                                                                 | 50  | 55  | 60  |     |
| TTT GGC AAC ACA ATC ACT TGT TAC ATC AAG GCC ACA ACG GCC GCG AAG |     |     |     | 238 |
| Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Thr Ala Ala Lys |     |     |     |     |
|                                                                 | 65  | 70  | 75  |     |
| GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTC TGC GGA GAT GAT CTG |     |     |     | 286 |
| Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp Leu |     |     |     |     |
|                                                                 | 80  | 85  | 90  | 95  |
| GTC GTG GTG GCT GAG AGT GAT GGC GTC GAC GAG GAT AGA GCA GCC CTG |     |     |     | 334 |
| Val Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Ala Ala Leu |     |     |     |     |
|                                                                 | 100 | 105 | 110 |     |
| AGA GCC                                                         |     |     |     | 340 |
| Arg Ala                                                         |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

|                                                                 |     |     |     |    |
|-----------------------------------------------------------------|-----|-----|-----|----|
| Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln |     |     |     |    |
| 1                                                               | 5   | 10  | 15  |    |
| Cys Cys Asn Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ser Leu Thr |     |     |     |    |
|                                                                 | 20  | 25  | 30  |    |
| Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Ala Gln |     |     |     |    |
|                                                                 | 35  | 40  | 45  |    |
| Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe |     |     |     |    |
|                                                                 | 50  | 55  | 60  |    |
| Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Thr Ala Ala Lys Ala |     |     |     |    |
|                                                                 | 65  | 70  | 75  | 80 |
| Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp Leu Val |     |     |     |    |
|                                                                 | 85  | 90  | 95  |    |
| Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Ala Ala Leu Arg |     |     |     |    |
|                                                                 | 100 | 105 | 110 |    |

Ala

## (2) INFORMATION FOR SEQ ID NO: 219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Glu | Gly | Arg | Thr | Ser | Trp | Ala | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

## (2) INFORMATION FOR SEQ ID NO: 220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Glu | Gly | Arg | Thr | Ser | Trp | Ala | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

## (2) INFORMATION FOR SEQ ID NO: 221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Thr | Glu | Gly | Arg | Thr | Ser | Trp | Ala | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

## (2) INFORMATION FOR SEQ ID NO: 222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 629 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 3..629

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 3..629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TA GAC TTT TGG GAG AGC GTC TTC ACT GGA CTA ACT CAC ATA GAT GCC  | 47  |
| Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala     |     |
| 1 5 10 15                                                       |     |
| CAC TTT CTG TCA CAG ACT AAG CAG CAG GGA CTC AAC TTC TCG TTC CTG | 95  |
| His Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu |     |
| 20 25 30                                                        |     |
| ACT GCC TAC CAA GCC ACT GTG TGC GCT CGC GCG CAG GCT CCT CCC CCA | 143 |
| Thr Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro |     |
| 35 40 45                                                        |     |
| AGT TGG GAC GAG ATG TGG AAG TGT CTC GTA CGG CTT AAG CCA ACA CTA | 191 |
| Ser Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu |     |
| 50 55 60                                                        |     |
| CAT GGA CCT ACG CCT CTT CTA TAT CGG TTG GGG CCT GTC CAA AAT GAA | 239 |
| His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu |     |
| 65 70 75                                                        |     |
| ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG GCA TGC ATG TCA | 287 |
| Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser |     |
| 80 85 90 95                                                     |     |
| GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG CTT GGA GGG GTC | 335 |
| Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu Gly Gly Val |     |
| 100 105 110                                                     |     |
| CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT TGT GTT GTG ATT | 383 |
| Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys Val Val Ile |     |
| 115 120 125                                                     |     |
| GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC GTT CCA GAC AAA | 431 |
| Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys |     |
| 130 135 140                                                     |     |

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|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG TGC TCA CAA GCT | 479 |
| Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys Ser Gln Ala |     |
| 145 150 155                                                     |     |
|                                                                 |     |
| GCC CCA TAT ATC GAA CAA GCT CAG GTA ATA GCT CAC CAG TTC AAG GAA | 527 |
| Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln Phe Lys Glu |     |
| 160 165 170 175                                                 |     |
|                                                                 |     |
| AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA CAA GCT GTC ATT | 575 |
| Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln Ala Val Ile |     |
| 180 185 190                                                     |     |
|                                                                 |     |
| GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG GCC TTT TGG CAC | 623 |
| Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala Phe Trp His |     |
| 195 200 205                                                     |     |
|                                                                 |     |
| AAG CAT                                                         | 629 |
| Lys His                                                         |     |

## (2) INFORMATION FOR SEQ ID NO: 223:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His |  |
| 1 5 10 15                                                       |  |
| Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu Thr |  |
| 20 25 30                                                        |  |
| Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser |  |
| 35 40 45                                                        |  |
| Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu His |  |
| 50 55 60                                                        |  |
| Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile |  |
| 65 70 75 80                                                     |  |
| Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala |  |
| 85 90 95                                                        |  |
| Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu Gly Gly Val Leu |  |
| 100 105 110                                                     |  |
| Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys Val Val Ile Val |  |
| 115 120 125                                                     |  |
| Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys Glu |  |
| 130 135 140                                                     |  |

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Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys Ser Gln Ala Ala  
145 150 155 160

Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln Phe Lys Glu Lys  
165 170 175

Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln Ala Val Ile Glu  
180 185 190

Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala Phe Trp His Lys  
195 200 205

His

(2) INFORMATION FOR SEQ ID NO: 224:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 2..12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

Ile His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 225:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

Val Asn Tyr His Asn Thr Ser Gly Ile Tyr His Leu  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

Ile His Tyr Arg Asn Ala Ser Asp Gly Tyr Tyr Ile  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

Leu Gln Val Lys Asn Thr Ser Ser Ser Tyr Met Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

Val Trp Gln Leu Arg Ala Ile Val Leu His Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

Val Tyr Glu Ala Asp Tyr His Ile Leu His Leu  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

Val Tyr Glu Thr Asp Asn His Ile Leu His Leu  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

Val Tyr Glu Thr Glu Asn His Ile Leu His Leu  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO: 236:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

Val Phe Glu Thr Val His His Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

Val Phe Glu Thr Glu His His Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

Val Phe Glu Thr Asp His His Ile Met His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

Val Tyr Glu Thr Glu Asn His Ile Leu His Leu  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 240:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

Val Tyr Glu Ala Asp Ala Leu Ile Leu His Ala  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 241:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

Val Gln Asp Gly Asn Thr Ser Ala Cys Trp Thr Pro Val  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 242:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 243:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

Val Arg Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Ile Ala Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Ile Ala Leu

1

5

10

## (2) INFORMATION FOR SEQ ID NO: 247:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

Val Lys Thr Gly Asn Ser Val Arg Cys Trp Ile Pro Leu  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

Val Lys Thr Gly Asn Val Ser Arg Cys Trp Ile Ser Leu  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 249:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

Val Arg Lys Asp Asn Val Ser Arg Cys Trp Val Gln Ile  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 250:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

Ala Pro Ser Phe Gly Ala Val Thr Ala Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

Val Ser Gln Pro Gly Ala Leu Thr Lys Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 252:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

Val Lys Tyr Val Gly Ala Thr Thr Ala Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 253:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

Ala Pro Tyr Ile Gly Ala Pro Val Glu Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 254:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

Ala Gln His Leu Asn Ala Pro Leu Glu Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 255:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

Ser Pro Tyr Val Gly Ala Pro Leu Glu Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 256:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

Ser Pro Tyr Ala Gly Ala Pro Leu Glu Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids



- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Tyr | Leu | Gly | Ala | Pro | Leu | Glu | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Tyr | Leu | Gly | Ala | Pro | Leu | Glu | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Tyr | Val | Gly | Ala | Pro | Leu | Glu | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Asn Val Pro Tyr Leu Gly Ala Pro Leu Thr Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Ala Pro His Leu Arg Ala Pro Leu Ser Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Ala Pro Tyr Leu Gly Ala Pro Leu Thr Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

Arg Pro Arg Gln His Ala Thr Val Gln Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 264:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Pro | Gln | His | His | Lys | Phe | Val | Gln | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

(2) INFORMATION FOR SEQ ID NO: 265:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Pro | Arg | Arg | Leu | Trp | Thr | Thr | Gln | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

(2) INFORMATION FOR SEQ ID NO: 266:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Pro | Arg | Ile | His | Glu | Thr | Thr | Gln | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

Thr Ile Ser Tyr Ala Asn Gly Ser Gly Pro Ser Asp Asp Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

Ser Arg Arg Gln Pro Ile Pro Arg Ala Arg Arg Thr Glu Gly Arg Ser  
1 5 10 15

Trp Ala Gln

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1443

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..1443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

ACC ATC ACC ACC GGA GCT TCT ATC ACA TAC TCC ACT TAC GGC AAG TTC  
Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe

48

| 1                                                               | 5 | 10  | 15  |     |
|-----------------------------------------------------------------|---|-----|-----|-----|
| CTT GCT GAT GGA GGG TGT TCA GGC GGC GCG TAT GAC GTG ATC ATA TGC |   |     |     | 96  |
| Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys |   |     |     |     |
| 20                                                              |   | 25  | 30  |     |
| GAC GAG TGC CAT TCC CAG GAC GCC ACC ACC ATT CTT GGG ATA GGC ACT |   |     |     | 144 |
| Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr |   |     |     |     |
| 35                                                              |   | 40  | 45  |     |
| GTC CTT GAC CAG GCA GAG ACG GCT GGA GCT AGG CTC GTC GTC TTG GCC |   |     |     | 192 |
| Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala |   |     |     |     |
| 50                                                              |   | 55  | 60  |     |
| ACG GCC ACC CCT CCC GGC AGT GTG ACA ACG CCC CAC CCC AAC ATC GAG |   |     |     | 240 |
| Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu |   |     |     |     |
| 65                                                              |   | 70  | 75  | 80  |
| GAA GTG GCC CTG CCT CAG GAG GGG GAG GTT CCC TTC TAC GGC AGA GCC |   |     |     | 288 |
| Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala |   |     |     |     |
| 85                                                              |   | 90  | 95  |     |
| ATT CCC CTT GCT TTT ATA AAG GGT GGT AGG CAT CTC ATC TTC TGC CAT |   |     |     | 336 |
| Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His |   |     |     |     |
| 100                                                             |   | 105 | 110 |     |
| TCC AAG AAA AAA TGT GAT GAA CTC GCC AAG CAA CTG ACC AGC CTG GGC |   |     |     | 384 |
| Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr Ser Leu Gly |   |     |     |     |
| 115                                                             |   | 120 | 125 |     |
| GTG AAC GCC GTG GCA TAT TAT AGA GGT CTA GAC GTC GCC GTC ATC CCC |   |     |     | 432 |
| Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala Val Ile Pro |   |     |     |     |
| 130                                                             |   | 135 | 140 |     |
| ACA GCA GGA GAC GTG GTC GTG TGC AGC ACC GAC GCG CTC ATG ACG GGA |   |     |     | 480 |
| Thr Ala Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu Met Thr Gly |   |     |     |     |
| 145                                                             |   | 150 | 155 | 160 |
| TTC ACC GGC GAC TTT GAT TCT GTC ATA GAC TGC AAC TCC GCC GTC ACT |   |     |     | 528 |
| Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser Ala Val Thr |   |     |     |     |
| 165                                                             |   | 170 | 175 |     |
| CAG ACG GTG GAC TTC AGT CTG GAT CCC ACT TTT ACC ATT GAG ACT ACC |   |     |     | 576 |
| Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr |   |     |     |     |
| 180                                                             |   | 185 | 190 |     |
| ACA GTG CCC CAG GAC GCA GTG TCC AGA AGC CAG CGT AGG GGC CGC ACG |   |     |     | 624 |
| Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr |   |     |     |     |
| 195                                                             |   | 200 | 205 |     |
| GGG AGA GGT AGG CAC GGC ATA TAC CGG TAT GTC TCG GCT GGA GAG AGA |   |     |     | 672 |
| Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala Gly Glu Arg |   |     |     |     |
| 210                                                             |   | 215 | 220 |     |
| CCG TCT GAC ATG TTC GAC TCC GTG GTG CTC TGT GAG TGC TAC GAT GCC |   |     |     | 720 |
| Pro Ser Asp Met Phe Asp Ser Val Val Leu Cys Glu Cys Tyr Asp Ala |   |     |     |     |
| 225                                                             |   | 230 | 235 | 240 |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| GGA TGT GCG TGG TAT GAT CTG ACT CCT GCC GAG ACT ACC GTG AGG TTG | 768  |
| Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr Val Arg Leu |      |
| 245 250 255                                                     |      |
| CGC GCT TAC ATA AAC ACC CCC GGG CTC CCT GTC TGT CAG GAC CAT TTG | 816  |
| Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu |      |
| 260 265 270                                                     |      |
| GAA TTC TGG GAG GGG GTG TTC ACG GGG CTC ACT AAC ATC GAC GCT CAC | 864  |
| Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile Asp Ala His |      |
| 275 280 285                                                     |      |
| ATG CTG TCA CAG ACC AAA CAG GGT GGG GAG AAT TTC CCA TAC CTT GTA | 912  |
| Met Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Phe Pro Tyr Leu Val |      |
| 290 295 300                                                     |      |
| GCG TAC CAA GCA ACA GTC TGT GTT CGC GCG AAA GCG CCC CCC CCC AGC | 960  |
| Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro Pro Pro Ser |      |
| 305 310 315 320                                                 |      |
| TGG GAC ACA ATG TGG AAA TGC ATG CTC CGT CTC AAA CCG ACT TTA ACT | 1008 |
| Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro Thr Leu Thr |      |
| 325 330 335                                                     |      |
| GGC CCT ACT CCC CTC TTG TAC AGG CTG GGG CCC GTC CAG AAT GAG ATC | 1056 |
| Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile |      |
| 340 345 350                                                     |      |
| ACA CTG ACG CAC CCC ATC ACC AAG TAC ATT ATG GCT TGC ATG TCT GCG | 1104 |
| Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala |      |
| 355 360 365                                                     |      |
| GAC TTG GAG GTC ATT ACC AGC ACT TGG GTT CTG GTG GGG GGC GTT GTG | 1152 |
| Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val |      |
| 370 375 380                                                     |      |
| GCG GCC CTG GCG GCC TAC TGC TTG ACG GTG GGT TCG GTA GCC ATA GTC | 1200 |
| Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val |      |
| 385 390 395 400                                                 |      |
| GGT AGG ATC ATC CTC TCT GGG AAA CCT GCC ATC ATT CCC GAT AGG GAG | 1248 |
| Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu |      |
| 405 410 415                                                     |      |
| GCA TTA TAC CAG CAA TTT GAT GAG ATG GAG GAG TGC TCG GCC TCG TTG | 1296 |
| Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu |      |
| 420 425 430                                                     |      |
| CCC TAT ATG GAC GAG ACA CGT GCC ATT GCC GGA CAA TTC AAA GAG AAA | 1344 |
| Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys |      |
| 435 440 445                                                     |      |
| GTG CTC GGC TTC ATC AGC ACG ACC GGC CAG AAG GCT GAA ACT CTG AAG | 1392 |
| Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys |      |
| 450 455 460                                                     |      |
| CCG GCA GCC ACG TCT GTG TGG AAC AAG GCT GAG CAG TTC TGG GCC ACA | 1440 |
| Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Ala Thr |      |
| 465 470 475 480                                                 |      |

1443

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 481 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

[illegible]

225                      230                      235                      240  
 Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr Val Arg Leu  
                                  245                      250                      255  
 Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu  
                                  260                      265                      270  
 Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile Asp Ala His  
                                  275                      280                      285  
 Met Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Phe Pro Tyr Leu Val  
                                  290                      295                      300  
 Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro Pro Pro Ser  
 305                                   310                                   315                                   320  
 Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro Thr Leu Thr  
                                  325                                   330                                   335  
 Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile  
                                  340                                   345                                   350  
 Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala  
                                  355                                   360                                   365  
 Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val  
                                  370                                   375                                   380  
 Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val  
 385                                   390                                   395                                   400  
 Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu  
                                  405                                   410                                   415  
 Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu  
                                  420                                   425                                   430  
 Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys  
                                  435                                   440                                   445  
 Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys  
                                  450                                   455                                   460  
 Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Ala Thr  
 465                                   470                                   475                                   480  
 Tyr

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